

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number: 134616

TO: James Schultz

Location: rem/2d1/8/2c18

**Art Unit: 1635** 

Thursday, October 07, 2004

Case Serial Number: 10/054313

From: Alex Waclawiw

**Location: Biotech-Chem Library** 

**Rem 1A71** 

Phone: 272-2534

Alexandra.waclawiw@uspto.gov

Search Notes		
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This Processing to (1970)

STÍC-Biotech/ChemL	ib CRFE		134616	
From: Sent: To: Subject:	Schultz, James Wednesday, October 06, 20 STIC-Biotech/ChemLib Seq search 10/054,313	004 5:21 PM		
Hello, Please run a standard amii	no acid sequence search on S	EQ ID NO:1, including	g the interference databases.	
Thanks Doug Schultz  James Douglas Schult AU 1635 (Biotechnology) Patent Examiner United States Patent and Touristics (Office) REM 2D18 (Mail) REM 2C18 (571) 272-0763	z, PhD	-aa- 286 mej	RECEIVED  OCT -7 2004  ECH/CHEV. Division.	

Type of Search
NA Sequence: #
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Structure: #
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Other:

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Q00870 trypanosoma
Q9ust8 schizosacch
Q8dm24 synechococc
Q89uu3 bradyrhizob
Q8sub4 lactobacill
Q820f5 anabaena sp
Q7vm15 haemophilus
Q82xv8 nitrosomona
Q8it47 leishmania
Q81t47 leishmania
Q817t0 pseudomonas
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RESULT
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MGD; MGI:1335073; Rnasehl.

GO; GO:0003676; F:nucleic acid bi
GO; GO:0004523; F:ribonuclease H
InterPro; IPR009027; L9 N like.
InterPro; IPR002156; RNaseH.

Pfam; PF0075; TnaseH; 1.

SEQUENCE 285 AA; 31833 MW; 84
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Mus musculus (Mouse).
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Mammalia; Eutheria;
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                                                                                                                                                                 KEDFMELDELTQGMDIQWMHIPGHSGFVGNEEADRLAREGAKQSED
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Rodentia;
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Q8X142
Q88142
Q82851
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Pred. No. 8.7e
27; Mismatches
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Q7z101 recombinant
Q83162 murine leuk
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Q76630 human immun
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MEDLINE-96437509; PubMed-8840185;

Sawada K., Agata K., Eguchi G.;

"Characterization of terminally differentiated cel
categorizing cDNA clones derived from chicken lens
Int. J. Dev. Biol. 40:531-535(1996).

EMBL; D26340; BAA05532-1; -.

HSSP; Q04740; 1QHK.
G0; GO:0004521; F:ribonuclease H activity; IEA.
G0; GO:0004521; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaseH.
Pfam; PP00075; rnaseH; 1.

SEQUENCE 293 AA; 32499 MW; 2B86AD6DC722682B CF
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Q8BU23;
01-MAR-2003
01-MAR-2003
01-OCT-2003
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
mRNA, complete cds, clone CLFEST65.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                  Simile.
RNASEH1.
Mus musculus (Mouse).
Miarvota; Metazoa; Chordata; '
haria; Rodentia;
the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs."; Nature 420:563-573 (2002). EMBL; AK088032; BAC40109.1; -.
                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local :
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01-JUN-2003 (TREMBLrel. 24, L
01-OCT-2003 (TREMBLrel. 25, L
Hypothetical protein F59A6.9.
F59A6.9.
                                                                                                                                                                                                                                                EMBL; U4194; AA091712.1; ...

WormPep; F59A6.9; CE33660.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004523; F:ribonuclease H activity; IEA.

InterPro; IPR009027; L9 N like.

InterPro; IPR009156; RNaseH.
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GO; GO:0004523; F:ribonuclease H activity;
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
SEQUENCE 153 AA; 16922 MW; C9AA7E094274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD;
                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.", Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                   Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                            Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nhan M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence of C. elegans cosmid F59A6.";
itted (DEC-1995) to the EMBL/GenBank/DDBJ
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                     FYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFV------RKSASPEV
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  YYAVARGKQVGIYRTWNECKTQIDGFQNARFKKFATEAEARKFVADNMSVPGSKPVTPAV
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                                                                                                                                                                                   l protein.
251 AA; 2
                                                                                         Conservative
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Pred. No. 2.7e-
12; Mismatches
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Last annotation updat
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                                                                                    Score 491; DB 5;
Pred. No. 1.9e-37;
9; Mismatches 78
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                                                                                                                                                                                   CFE6AA1B5BE0DF9A CRC64;
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                                                                                                                                   Length 251;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D., RA Adams M.D., Celniker S.E., Holt R.A., Howkins R.A., Galle R.F., RA Adams M.D., Celniker S.E., Holt R.A., Howkins R.A., Galle R.F., RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.G., Champe M., Pfeiffer B.D., Chen L.X., Rayens P.C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Bakter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Baros P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Besnos P.V., Berman B.P., Bhandari D., Bolshakov S., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Dietz S.M., Dodoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., Roseler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Kimmel B.F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laing Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Liz, Liang Y., Lin X., Ra McInto G., Milshina N.V., Mobarry C., Morris J., Moshreti A., Ra Kinmel B.F., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Ra McInto M., Pittman G.S., Sangheton M., Skupski M.P., Pacleb J.M., Palacon D.L., Wei M., Pala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9V335;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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RESULT 6
044114
ID 0441
AC 0441
AC 0441
AC 0441
AC 0441
DT 01-J
DT 01-J
DT 01-G
DE Ribo
GN RNH1
OS Dross
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Best Local S
Matches 107
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01-JUN-1998
01-JUN-1998
01-OCT-2003
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Celniker S.;
melanogaster.";

Biochem. Biophys. Res. Commun.

Biochem. BAP032921; AAC47810.1; ..

EMBL; AF032921; JC5787.
                                                        MEDLINE-98063328; PubMed-9398656; Filippov V., Filippova M., Gill S.S.; Functional characterization of RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A2003339; AAF59170.1; -.
EMBL; A2003399; AAF59170.1; -.
HSSP; Q04740; 1QHK.
F1yBase; FBqn0023171; rnh1.
G0; G0:004524; F:ribonuclease H1 activity; IDA.
InterPro; IPR009027; L9 N like.
InterPro; IPR002156; RNaseH.
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                                                                                                    SEQUENCE FROM N.A. STRAIN=OREGON R;
                                                                                                                                         Neoptera; Endopterygota; Dir
Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                               Ribonuclease H1. RNH1 OR CG8729.
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                                                                                                                                                                                                                                                                                                                                                                 EMADKLARQGS
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(TrEMBLrel.
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AA; 37148 MW;
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25,
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                                240:844-849(1997).
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V., Park S.,
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RESULT 7
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AC 001-0
AC 0008
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Matches 106
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Best Local Similarity
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FlyBase; FBgn0023171; rnhl.

GO; GO:004524; F:ribonuclease H1 a.

InterPro; IPR009027; L9_N_like.

InterPro; IPR002156; RNaseH.

Pfam; PF00075; rnaseH; J.

SEQUENCE 333 AA; 37164 MW; D1801
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01-JUL-1997
01-OCT-2003
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                                                                                                                                                                                                EMBL; U74470; AAC47537.1; -.
HSSP; Q044740; LQHK.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0003676; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaeeH.
InterPro; IPR002156; RNaeeH.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              kinetoplastid, Trypanosoma brucei.";
Mol. Biochem. Parasitol. 86:121-126(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97321566; pubMed=9178276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=366D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa;
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribonuclease
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                                                                                                            Similarity
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|||| ||::||: :| || || ||::||| || || ||:|:
FYAVASGRRSGVYGSWAECEEQVKGFKNAKYKKFKTRQEADQFVNGCKSYAPQDVAVPLG
FYAVAVGRQTGVFSTWEECQKQVSGFSGARFKSFLTLQEAQAYA--SGVQDVDPGSVGTS
                                          FYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFVRKSASPEVSEGHENOH
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(TrEMBLrel.
e H1.
                                                                                      Conservative
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                                                                                  24.0%; Score 370.5; DB 5
34.8%; Pred. No. 4.1e-26;
Live 33; Mismatches 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinetoplastida;
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RESULT 8
Q9UST8
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-!- SIMILARITY BELONGS TO THE RNASE H FAMILY.
EMBL; AP048992; AAC043661; --
EMBL; AL121815; CABS8158.1; --
EMBL; A121815; CABS8158.1; --
EMBL; A04740; T40244.
HSSP; 004740; 104K.
GeneDB_SPombe; SPBC336.06C; --
GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:00016787; F:hydrolase activity; IEA.
GO; GO:00016787; F:magnesium ion binding; IEA.
GO; GO:0000287; F:magnesium ion binding; IEA.
GO; GO:0004524; F:ribonuclease H activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribonuclease H (EC 3.1.26.4) (RNase H)
RNH1 OR SPBC336.06C.
                     DOMAIN
VARIANT
                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=912;
Tozawa Y., Crouch R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UST8; 042798;
01-MAY-2000 (Tr
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic and cDNA sequences of Schizosaccharomyces pombe Ribonuclease
                                                                                           Pfam;
                                                                                                        InterPro; IPR009027; L9_N_like.
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS ENZYME IS AN ENDONUCLEASE THAT DEGRADES RNA-DNA HYBRIDS SPECIFICALLY.
CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOS
                                                                                                                                                                                                                                                                                                                                         COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                          MONOESTER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DFVAL------BRLT-------QGMDIQWMHVPGHSGFIGNEEADRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALIHVLRVALDSHPCYN---LCVYSDSKYTVMGVNSYLHRWERNGFKTAGGGDVANIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYMGDFVVVYTDGCCSSNG----RKKPRAGIGVYWGPGHPLNVGIRLPGR--QTNQRAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSQFTKLRNRHLSRCAERFTMEFRFKASLAAIAARAVALQLKHVPGHAGVYGNEMADRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- IHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVADSHTPVLVGVKRALSLDVTLDAVEVDAADDGNE-VDDESKQQVLSPEWVEARKREA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQESEAKP---GKRLREPLD------GDGHESAQPYAKHMKPSVEPAPPVSRDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGAK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VVVYVDGACRNNGSRSRERRPRAGFGGFYGDGDSRNFKFPLPAHEPQTNQRAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beck A., Reinhardt R., McDougall R.C., Rajandream
                                                                       Nuclease; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
     ;; Endonuclease; Magnesium; Metal-binding.
62 POLY-SER.
82 POLY-SER.
129 D -> E (IN STRAIN 912).
129 MAGNESIUM (BY SIMILARITY).
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POLY-SER.
D -> E (IN STRAIN 912).
MAGNESIUM (BY SIMILARITY).
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Q8DM24;
01-MAR-2003
01-MAR-2003
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; DNA Res. 9:123-130(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                     EMBL; AP005369; BAC07852.1; -.
GO; GO:0003676; F:nucleic acid binding; IE:
GO; GO:0004523; F:ribonuclease H activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus elongatus
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                 Pfam; PF00075; rnaseH; 1.
Complete proteome.
SEQUENCE 159 AA; 17790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNHA OR TLR0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribonuclease H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=32046;
                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                         198
                                                                                                                                              142
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                                                                       KTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQ
                                                                                                                                             VYTDGCCSSNGRRKPRA---GIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQ-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDLINRASDLMSDRNVSLEYVKGHSTDYGNQQADMLARRGASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KSASPEVSEGHENQHGQE-SEAKPGKRLREPLDGDGHESAQPYAKHMKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMHVPGHSGFIGNEEADRLAR 278
                                                                                                             IYTDGACEGN----PGPGGWGVVIYFTDGSVHELGGHHPA-TTNNRMELQAAIEALKAWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ
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                                        QLAPGSAIALYTDSEYVLRGITEWIHHWKRRGWKTAAKKPVLNQDLWQELDALNDPL-VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNNRAELQAIILALENTS----GDLTIRSDSNYSIKSLTTWLPKWKKNDFKTSNSQPVKN
                                                                                                                                                                                                                                                                                                      IPR002156; RNaseH.
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191
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191
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                                                                                                                                                                                                                                                     17790 MW;
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                                                                                                                                                                               15.8%; Score 245; DB 16; 37.6%; Pred. No. 8.4e-15; tive 26; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Thermosynechococcus elongatus); Chroococcales; Synechococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last
Last
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Pred. No. 8.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGNESIUM
MAGNESIUM
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AGNESIUM (BY SIMILARITY)
9B38CB344B731DE0 CRC64;
                                                                                                                                                                                                                                                     EE5900EC032931E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ikeuchi M., Katoh H., Sasamou
ima K., Kimura T., Kishida Y.,
n m. Matsuno A., Nakazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
annotation update)
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RESULT ID RESULT
RESULT 11
Q88UB4
ID Q88UE
AC Q88UE
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DT 01-J1
DT 01-J1
DT 01-O
GN RNH
OS LACT
OC Bact
OC Lact
OC Lact
CX NCS:
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01-JUN-2003
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Q89UU3;
01-JUN-2003
01-JUN-2003
01-OCT-2003
     SEQUENCE FROM N.A.
STRAIN-NCIMB 8826 / WCFS1;
MEDLINE-22480296; PubMed-12566566;
MEDLENE-22480296; PubMed-12566566;
Kleerebezem M., Boekhorst J., van Kranenburg
Kuipers O.P., Leer R., Tarchini R., Peters S.
Fiers M.W.E.J., Stiekema W., Klein Lankhorst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
MEDLINE=22484998; PubMed=12597275;
Medeko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                          Bacteria; Firmicutes; Lactobacillus.
                                                                                                                                                                                                                                                      RNH OR LP 2593.
Lactobacillus plantarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP005939; BAC46581.1; --
GO; GO:0003676; F:nucluic acid
GO; GO:0004523; F:ribonuclease
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphapro
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                          Ribonuclease H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 AA; 17264 MW;
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- u (Putative) (EC 3.1.26.4).
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25,
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Last sequence update)
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H activity;
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     R., Molenaar D.,
.A., Sandbrink H.M.,
R.M., Bron P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49; Indels
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   Query Match
Best Local
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Best Local Similarity
                                                                                                  Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe A., Iriguchi M., Ishikawa A., Kawash
Kishida Y., Kohara M., Matsumoto M., Matsumo J
Nakazaki N., Shimpo S., Sugimoto M., Takazawa
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8Z0F5;
01-MAR-2002
01-MAR-2002
01-OCT-2003
                                                                                                                                                                                          EMBL; AP003581; BAB77666.1; -.
PIR; AF1824; AF1824.
GO; GO:0003576; F:rnucleic acid binding; IEJ
GO; GO:0004523; F:ribonuclease H activity;
InterPro; IPR002156; RNaseH.
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GO; GC:0016787; F:hydrolase activity; IEA.
GO; GC:0003576; F:nucleic acid binding; IEA.
GO; GO:0003576; F:ribonuclease H1 activity;
InterPro; IPR00915; L9_N like.
InterPro; IPR00915; RNaseH.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.", DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anabaena sp. (strain PCC Bacteria; Cyanobacteria; Cronobacteria; CRBI_TaxID=103690;
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ALR0142.
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SEQUENCE
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                                                                                                                                                                  Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
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                                                                                                                                                              PF00075; rnaseH; 1.
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298 AA; 33023 MW;
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Nostocales;
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Pred. No. 4.6e-14;
   Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Kuritz T., Sasamoto :
a A., Kawashima K., Ki
M., Matsuno A., Muraki
M., Takazawa M., Yamad
   238;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nostocaceae; Nostoc
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8.9e-14;
                                                                                                                                                                                                              IEA.
IEA.
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RESULT 14
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Probable ribonuclease hi protein (ERNHA OR NE0140.
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SEQUENCE
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MUNBON R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
  SEQUENCE FROM N.A.
STRAIN=ATCC 19718 /
MEDLINE=22586410; P
                                                                            NCBI_TaxID=915;
                                                                                                                        Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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Pasteurellaceae; Haemophilus.
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153 AA;
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  / IFO 14298;
PubMed=12700255;
                                                                                                       Nitrosomonas
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Pred. No. 1.2e
19; Mismatches
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Q8IT47;
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AF542055; AAN17340.1; -.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
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Eukaryota; Euglenozoa;
EURI_TaxID=5664;
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01-MAR-2003 (TrEMBLrel. 23,
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GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004524; F:ribonuclease H1 activity; IEA
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Hydrolase; Complete prote
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"Cloning and characterization of ribonuclease HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                            I SWHWVRGHNGHPGNERADALANRG
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AA; 16238 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                      ; Score 219.5; |
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20; Mismatches
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MEDINE=22423060; PubMed=12534463;
Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert Martins dos Santos V.A.P., Fotts D.E., Gill S.R., Pop M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J Madupu R., Nelson W., White O., Peterson J., Khouri H., Ha Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedl Lauber J., Stjepandic D., Hohelsel J., Straetz M., Heim S. Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemml
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SEQUENCE
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Bacteria; Proteobacteria; Gammaprot
Pseudomonadaceae; Pseudomonas.
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GO; GO:0004523; F:ribonuclease
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain (Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Hollroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
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GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaseH.
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Nature 413:484-852 (2001).
EMBL; AL513384; CAD09976.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhi.
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                                                                                                                                                                                                                                                                                                                                                                 Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pHCM2
                                                                                                                                                                      InterPro; IPR002156; RNaseH.
                                                                                                                                                                                          L; AL513384; CAD09976.1; -
GG:0046821; C:extrachromosomal
GO:0003676; F:nucleic acid bind
GO:0004523; F:ribonuclease H ac
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                                                                                             PF00075; rnaseH; 1.
id; Complete proteom
NCE 202 AA; 23149
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Pred. No. 2.2e
21; Mismatches
Score 214; DB
Pred. No. 8.9e
26; Mismatches
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                                                                                               CAF9ECOA155E8ED9 CRC64;
                                                                                                                                                                                             activity;
                                                                                                                                                                                                                                             DNA;
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RESULT 19
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ID Q7WCJ8
RESULT 20
Q7W0T2
ID Q7W0T
AC Q7W0T
DT 01-OC
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A Parkhill J., Sebalhia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Chillingworth T., Collins M., Cronnin A., Davis P., Doggett J.,

A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

A Leather S., Mutter S., Sanders M., Saunders D., Seeger K.,

A Leather S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Q7W0T2;
Q7W0T2;
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7WCJ8;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequen
01-OCT-2003 (TrEMBLrel. 25, Last annota
Ribonuclease HI (EC 3.1.26.4).
DASF OR HERA OR RNH OR RNHA OR SDRA OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BX640450; CAE34642.1; -. Hydrolase; Complete proteome. SEQUENCE 155 AA; 17455 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RB50 / ATCC BAA-588;
MEDLINE=22827954; PubMed=12
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Last annotation update)
                            Created)
Last sequence update)
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Pred. No. 1.6e-11;
5; Mismatches 63
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APARTHIB-22827954; PubMed=12910271;
APARTHIB-22827954; PubMed=12910271;
APARTHIB-22827954; PubMed=12910271,
APARTHIB-22827954; PubMed=12910271,
APARTHIB-D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
APARTHIB-D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
APARTHIB-D.E., Holden M.T.G., Basham D., Bason N., Cherevach I.,
APARTHIB-D.E., Collins M., Cronin A., Davis P., Doggett J.,
APARTHIB-D.E., Collins M., Cronin A., Davis P., Doggett J.,
APARTHIB-D.E., Moule S., Namlin N., Hauser H., Holroyd S., Jagels K.,
APARTHIB-D.E., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
APARTHIB-D.E., Standers M., Saunders D., Seeger K.,
APARTHIB-D.E., Standers M., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Mainonds M., Skelton J., Squares R., Squares S., Stevens K.,
APARTHIB-D.E., Comparative and Bordetella bronchiseptica.";
APARTHIB-D.E., CARS9117.1;
APARTHIB-D.E., C
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Best Local S
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Query Match
Best Local Similarity
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Q7VQB6;
01-OCT-2003
01-OCT-2003
                                                                                                                                   MEDLINE-22794745; PubMed=12886019;
Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
van Ham R.C.H.J., Gross R., Moya A.;
"The genome sequence of Blochmannia floridanus: comparative analysis
of reduced genomes.";
Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
EMBL; BX246584; CADB3738.1; -.
Hydrolase; Complete proteome.
SEQUENCE 167 AA; 19480 MW; 3071B72795CC30ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Ribonuclease H (EC 3.1.26.4).
RNHA OR BFL224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
NCBI_TaxID=203907;
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Alcaligenaceae; Bordetella.
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DASF OR HERA OR RNH OR RNHA OR SDRA OR BPP3834.
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SEQUENCE
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STRAIN=12822 / ATO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HQVQWRWVRGHAGDPGNERADALANQGVE
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155 AA; 17455 MW;
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13.5%;
36.1%;
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Pred. No. 1.6e
25; Mismatches
Score 209; DB 1
Pred. No. 2e-11;
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                                               DB 16;
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                                               Length 167;
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Best Local S
Matches 57
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                                                                                         Q7VRX8;
Q7VRX8;
01-OCT-2003
01-OCT-2003
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                                           01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribonuclease HI (EC 3.1.26.4).
DASF OR HERA OR RNH OR RNHA OR SDRA OR BP3211.
Borderella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                   Bacteria; Proteobacteria;
Alcaligenaceae; Bordetella
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EMBL; BX572101; CAE22267.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22825698; PubMed=12917642;
ROCED G., LEXIMET F.W., LEMERGIN J.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible ribonuclease HI (EC 3.1.26.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome divergence in two Prochlorococcus ecotypes niche differentiation.";
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                                                                                                                                                                                                                         118 AR--LD----HVPLAYVKGHSGDPDNERVDQIA 144
                                                                                                                                                                                                                                                                                                            191 CKAIEQAKTQNIN-KLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALER
                                                                                                                                                                                                                                                                                                                                                                    137 GDFVVVYTDGCCSSNGRRKPRAGIGVYWG-----PGHPLNVGIRLPGRQTNQRAEIHAA
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                                                                                                                                                                                                                                                      LTQGMDIQWMHVP----GHSGFIGNEEADRLA 277
                                                                                                                                                                                                                                                                                 LHVLEQLKELPCHPDLKIRTDSKYLIDGLSKWMAGWKRKGWRTAAGKPVLNQDLWRALDR
                                                                                                                                                                                                                                                                                                                                        GRVVAAATDGACSGN----PGPG---GWGALLRFEDGSVEEFGGYAPA-TTNNRMELQAA
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257 AA; 28057 MW;
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                    PRELIMINARY;
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                   Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                              13.5%; Sco
37.3%; Pro
ative 20;
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                                 Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                              Score 209; DB 16; Length 2
Pred. No. 3.6e-11;
20; Mismatches 50; Indels
                                                                                                                                                    PRT;
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RC MEDLINE=22827954; PubMed=12910271;

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Heather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Unwin L., Whitchead S., Barraell B.G., Waskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapertussis and Bordetella bronchiseptica.";

RT Bordetella parapertussis and Bordetella bronchiseptica.";

RM Busk (Genet. 35:32-40(2003).

DR EMBL; BX640420; CAE43477.1;

EMBL; BX640420; CAE43477.1;

RT BX6 (Genet. 35:32-40(2003).
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Palenik B., Brahamsha B., Larimer F.W., Land M.,
Lamerdin J., Regala W., Allen E.E., McCarren J.,
Dufresne A., Partensky F., Webb E.A., Waterbury
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
EMBL, BX569695; CAE08853.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT 2003 (TrEMBLrel 25, 0
01-OCT-2003 (TrEMBLrel 25, 1
01-OCT-2003 (TrEMBLrel 25, 1
Possible ribonuclease HI (EC
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNHA OR SYNW2338.
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122
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                                                                                                   GRVVAAATDGACSGN----PGPG---GWGALLRFEDGSVEEFGGHDPA-TTNNRMELQAA
                                                                                                                                                            GDFVVVYTDGCCSSNGRRKPRAGIGVYWG-----PGHPLNVGIRLPGRQTNQRAEIHAA
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(TrEMBLrel. 25, Last sequence up
(TrEMBLrel. 25, Last annotation
bonuclease HI (EC 3.1.26.4).
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                   27400 MW;
                                                                                                                                                                                                                      13.5%; Score 208; DB 16; 36.7%; Pred. No. 4.3e-11; tive 23; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 208.5; 34.0%; Pred. No. 2e-: tive 24; Mismatches
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Paulsen I.,
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QBEE30;
Q1-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPRO02156; RNaseH.
Pfam; PF00075; rnaseH; 1.
Complete proteome.
SEQUENCE 158 AA; 17782 MW; BDEBAE51CC162E4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
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                                                                                                                                                                                                                       EP--CKIILTSDSQYMRQGIMTWIHGWKKKKGWMTSNRTPVKNVDLWKRLDKAAQLHQIDW
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 203.5; DB 16; Length 158; 35.4%; Pred. No. 6.1e-11; tive 19; Mismatches 63; Indels 11;
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O60930 homo sapien
O70338 mus musculu
Q07762 crithidia f
Q04740 saccharomyc
P57813 pasteurella me
P57813 pasteurella me
P43807 haemophilus
Q995841 rhizobium I
Q91289 pseudomonas
Q99145 neisseria m
Q99195 neisseria m
Q99194 zymomonas m
Q92rg0 rhizobium m
Q92rg0 rhizobium m
Q92rg0 rhizobium m
Q92rg1 zagrobacteri
Q9341 caulobacter
Q9341 caulobacter
Q8741 pseudomonas
Q80ff5 pseudomonas
Q80ff2 pseudomonas
Q80ff3 presinia pe
Q8x291 ralstonia s
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Q8x291 ralstonia pe
Q8x291 ralstonia pe
Q8x291 rabrio chol
Q8dbd5 vibrio vuln
P00647 escherichia
Q8ff7 photorhabdu
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POL HV2SI
POL FIVE
POL HV2SI
POL HV2NZ
POL FIVE
POL SIVAI
POL SIVA
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Result No.

Minimum Maximum

Database

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Former A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEbwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Balesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Foc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                            CHARACTERIZATION.

MEDLINE=99428493; PubMed=10497183;

Wu H., Lima W.F., Crooke S.T.;

"Properties of cloned and expressed human RNase H1.";

J. Biol. Chem. 274:28270-28278(1999).

-!- FUNCTION: This enzyme is an endonuclease that degrades
RNA-DNA hybrids specifically.

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                  Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribonuclease H1 (EC 3.1.26.4) PRT; 2

Rival HUMAN STANDARD; PRT; 2

060930; 060923; 0609857;
16-0CT-2001 (Rel. 40, Last sequence up
10-0CT-2003 (Rel. 42, Last annotation
Ribonuclease H1 (EC 3.1.26.4) (RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
 Thie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98171047; pubMed=9512096;
Wu H., Lima W.F., Crooke S.T.;
"Molecular cloning and expression of cDNA for l
"Notesense Nucleic Acid Drug Dev. 8:53-61(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99017966; PubMed=9799596; Cerritelli S.M., Crouch R.J.;
                               -!- SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                        phosphomooester.

COFACTOR: Binds 1 magnesium ion per
COFACTOR: REGULATION: In the presence
                                                 SUBUNIT: Monomer (Probable).
SUBCELLULAR LOCATION: Cytoplasm
TISSUE SPECIFICITY: Ubiquitous
                                                                                                      ENZYME REGULATION: inhibitory.
 SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCE FROM N.A.
P., Braunshofer-Reiter C.,
ing and functional expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  telli S.M., Crouch R.J.;
ing, expression, and mapping of ribonucleases
related to bacterial RNase HI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53:300-307(1998).
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 18
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expression of human RNase HII.";
the EMBL/GenBank/DDBJ databases.
copyright.
                                                                   Cytoplasmic
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H1) (Ribo
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                                                                     (Potential)
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of magnesium,
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produced
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through
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collaboration
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                                                                                                                                                                                                                             RNH1 MOUSE
070338;
16-OCT-2001
16-OCT-2001
28-FEB-2003
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METAL
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                       LT 2
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as all secontent is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q04740; 1QHK.
Genew; HGNC:18466; RNASEH1.
MIM; 604123; -.
                                                                                                                                                                                         RNASEH1 OR RNH1.
                                                                                                                                                                                                            Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004540; F:ribonuclease act
GO; GO:006401; p:RNA catabolism;
InterPro; IPR009027; 19, M like.
InterPro; IPR002156; RNaseH.
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GO; GO:0006401;
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                                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
H1 (EC 3.1.26.4) (RNase H1).
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186
210
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Rodentia;
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MAGNESIUM (BY SIMILARITY).
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
L -> F (IN REF. 1).
Q -> R (IN REF. 3).
Q -> R (IN REF. 3).
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Pred. No. 6
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                    PRT;
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TISSUE=Carcinoma;
MEDLINE=99017966; PubMed=9799596;
Cerritelli S.M., Crouch R.J.;

SEQUENCE

FROM N

NCBI\_TaxID=10090

Mus

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RAUSULT 3
RNH1 CRIFA
ID RNH1 CRIFA
AC 007762;
DT 01-0CT-1994
DT 01-0CT-1994
DT 28-FEB-2003
DE RIBDICAL REBORNH1.
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Best Local Similarity
RNH1.
Crithidia fasciculata.
Eukaryota; Euglenozoa; I
NCBI_TaxID=5656;
                                                                                                                                                        01-OCT-1994
01-OCT-1994
28-FEB-2003
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METAL 144 144 MAGNESIUM (BY SIMILARITY).

METAL 185 185 MAGNESIUM (BY SIMILARITY).

METAL 209 209 MAGNESIUM (BY SIMILARITY).

METAL 273 273 MAGNESIUM (BY SIMILARITY).

SEQUENCE 285 AA; 31805 MW; 92B09F8EFAFA822F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage t
                                                                                                                               Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF048993; AAC78562.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1335073; Rnaseh1
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SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphomonoester.

COPACTOR: Binds 1 magnesium ion per subunit (By similarity)

ENZYME REGULATION: In the presence of magnesium, manganese
inhibitory (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
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                                                                                                                                                                                                                                                                                                                                                                                                 KEDFMELDELTQGMDIQWMHIPGHSGFVGNEEADRLAREGAKQSED
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                                                                                                                            (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 41, Last annotation updat
H (EC 3.1.26.4) (RNase H).
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77.3%;
                                                    Kinetoplastida; Trypanosomatidae; Crithidia.
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Pred. No. 8.46
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RNHI\_YEAST Q04740; Q04740; 01-OCT-1993 (Rel. 27, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation updat

update)

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Pfam; PF00075; rnaseH; 1.
Hydrolase; Nuclease; Endonuclease; Magnesium.
Hydrolase; Nuclease; Endonuclease; Magnesium (BY SIMILI
METAL 281 281 MAGNESIUM (BY SIMILI
METAL 325 325 MAGNESIUM (BY SIMILI
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METAL 374 374 MAGNESIUM (BY SIMILI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C1;
MEDLINE=94022373; PubMed=8415705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L18916; AAA03546.1; -. PIR; A48683; A48683. HSSP; Q04740; 1QHK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Proc. Natl. Acad. Sci. U.S.A. 90:9350-9354(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional complementation of an Esch mutation by a cloned genomic fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campbell A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q04740; 1QHK.
InterPro; IPR009027; L9_N_like.
InterPro; IPR002156; RNaseH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the RNase H family.
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COFACTOR: Binds 1 magnesium ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Endonucleolytic
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98; Conserv
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TDSRYVIDGLTRYALKWVANGFKLASKEPVLNQDLWRQLIRLRDAYNTRYAEQQHWAAAT
                                                                                                                                                  TDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERL-------
                                                                                                                                                                                                          VPITEAQTNINGEMRAVIHCIVQGFVDAGVPPAALGTSHCVEPDWELSELPQPLRRLVIY
                                                                                                                                                                                                                                                          IRLPGRQTNQRABIHAACKAIEQA-----
                                                                                                                                                                                                                                                                                                            VEEEVPSGAAAVQRAESSVP----QVVYVDGACSHNGTPKARAGYGGFYGSTSDSRNFSLP
                                                                                                                                                                                                                                                                                                                                                            KPSVEP--APPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWG---PGHPLNVG
                                                                                                                                                                                                                                                                                                                                                                                                                  YL--TAHPARSGLEKSDRGDGAASLSALSEPQVGLRRSRAAEAEASYVVEAPAQPTLRQR
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Pred. No. 6.2e-19;
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                                               TOGMDIOWMHVPGHSGFIGNEEADRLAREGAK 282
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Query Match
Best Local Similarity
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SEQUENCE
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Bowman S., Churcher C.M., Badcock K., Brown D., Chill Bowman S., Dedman K., Devlin K., Gentles S., Hamlin N Jagels K., Lye G., Moule S., Odell C., Pearson D., Ra Rice P., Skelton J., Walsh S., Whitehead S., Barrell "The nucleotide sequence of Saccharomyces cerevisiae
                                                                                                                       METAL
METAL
                                                                                                                                                                                Germonline; 142909; -.
SGD; S0004847; RNHI.
SGD; GO:0004523; F:ribonuclease
GO; GO:0007047; P:cell wall org
InterPro; IPR009027; L9 N like.
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                       EMBL; Z49939; CAA90205.1;
EMBL; X57160; CAA40448.1;
PIR; S57601; S57601.
PDB; 1QHK; 31-AUG-99.
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evans S.P., Bycroft M.; "NMR structure of the N-terminal domain of Saccharomyces RNase HI reveals a fold with a strong resemblance to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Itaya M., McKelvin D., Chatterjie S.K "Selective cloning of genes encoding I typhimurium, Saccharomyces cerevisiae
                                                                                                                                               Hydrolase;
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain of ribosomal protein L9.";
J. Mol. Biol. 291:661-660/1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evans S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99380410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 157-348 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 6-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91326035; PubMed=1650910
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the RNase
                                                                                                                                                                                                                                                                                                                                                                                                                             phosphomonoester.
COFACTOR: Binds 1 magnesium ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR YMR234W
                                                                                                                                                                       PF00075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ces cerevisiae (Baker's yeast).
Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
cetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                            Nuclease;
                                      348
                                                  235
264
338
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17
22
38
43
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235
264
338
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39431 MW;
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                                                                                                         Endonuclease; Magnesium; 3D-struc
93 MAGNESIUM (BY SIMILARITY)
35 MAGNESIUM (BY SIMILARITY)
64 MAGNESIUM (BY SIMILARITY)
38 MAGNESIUM (BY SIMILARITY)
  16.1%;
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                                                                                                                                                                                                        organization
 Score
Pred.
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                                    02403B2329126B90 CRC64;
                                                                                                                                                                                                        activity; IDA.
nization and biogenesis; IMP
 249.5;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  per subunit.
e H family.
1.1e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crouch R.J.;
ase H from Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cleavage
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            Length 348;
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chromosome
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N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNH PASMU STANDZ
P57813;
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
15-MAR-2004 (Rel. 43,
Ribonuclease HI (EC;
 Hydrolase;
METAL
METAL
METAL
                              InterPro; lrkuvanie, 1.
Pfam; PF00075; rnaseH; 1.
"""rolase; Nuclease; Endc
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      MADILINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl Acad Sci. U.S.A. 98:3460-3465(2001).

-- FUNCTION: This enzyme is an endonuclease that de RNA-DNA hybrids specifically (By similarity).

--- CATALYTIC ACTIVITY: Endonucleolytic cleavage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gam
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNHA OR RNH OR PM0107. Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Pm70;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                phosphomonoester.

COPACTOR: Binds 1 magnesium ion per subunit (B: SUBUNIT: Monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Potential).

SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236
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                                                                                                              AE006046; AAK02191.1;
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                                                                  MF_00042; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFVRK------S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1EAVSEALKKIWEKLTNEKEKVNYQIKTDSEYVTKLLNDRYMTYDNKKLEGLPNSDLIVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHAACKAIEQ--AKTQNINKLVLY---TDSMFTINGITNWVQGWKKNGWKTSAGKEVI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSNTM---YNKSMNVYCDGSSFGNGTSSSRAGYGAYFEGAPEENISEPLLSGAQTNNRAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGQVSKPHTTQ-----KRVHRRNRPLHYSSLTSSSACSSLSSANTNTFYSVKSNVPN
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; Endonuclease; N
10 MAGNES
48 MAGNES
70 MAGNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -NKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria;
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 lease; Magnesium; Complete
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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1 Pm70.";
                                                                                                                                                                                                                                                                                             similarity).
                                          proteome.
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RESULT 6
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083372;

30-MAY-2000 (Rel. 3

30-MAY-2000 (Rel. 3

28-FEB-2003 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Braser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey B.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Sodergren E., Hardham J., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
SEQUENCE
                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                           HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
                                                                                                                     EMBL; AE001215; AAC65340.1; PIR; G71333; G71333.
                                                                                                                                                                                                                                                                                                                                                                                                           Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum.
Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNHA OR TP0353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribonuclease H (EC
Hydrolase; Nuclease; Endonuclease; Magnesium; Complete proteome.
METAL 12 12 MAGNESIUM (BY SIMILARITY).
METAL 63 63 MAGNESIUM (BY SIMILARITY).
                                                                                         HSSP; P00647; 1RBS.
TIGR; TP0353; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98332770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                  COFACTOR: Binds 1 magnesium ion per subunit (By SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                          FUNCTION: This enzyme is an endonuclease that degrades RNA-DNA hybrids specifically (By similarity). CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                              phosphomonoester.
COFACTOR: Binds 1
                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the RNase H family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAVIEALNTLKEP--CSVTLHSDSQYMKNGITKWIFNWKKUNWKASTGKPVKNQDLWIQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39, Created)
39, Last sequence update)
41, Last annotation updat
iC 3.1.26.4) (RNase H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGNESIUM (BY SIMILARITY).; 37A58196EA7661BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       Jablonski L., Larsen N., D'Souza M., Bernal A., Mujer C., Lo
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular nather Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRUME
                                                                                                                                        animal and plant pathogens and symbionts.",

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

-I- FUNCTION: This enzyme is an endonuclease that d.

RNA-DNA hybrids specifically (By similarity).

-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=B.melitensis; STRAIN=16M / MEDLINE=20020109; PubMed=11756688; MEDICINE=20020109; PubMed=1756688; MEDICINE (N.G., Kapatral V., Redking)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L5-MAR-2004 (Rel. 43, Last annotation upon Ribonuclease HI (EC 3.1.26.4) (RNase HI) RNHA OR BMEI1457 OR BR0477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
METAL
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                              Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Baugherty S.C., Deboy R.T., Durkin A.S., Kolomay J.F., Madupu Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Al Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L. Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C. "The Brucella suis genome reveals fundamental similarities bet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brucella melitensis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNH_BRUME
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003
                                                                                                                                                                                                                                                                                                   MEDLINE=22247741; PubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=29459,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                 phosphomonoester.

COFACTOR: Binds 1 magnesium ion per subunit
SUBUNIT: Monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Potential
                                                                     SIMILARITY: Belongs to the RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
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(BY SIMILARITY)
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Fraser C.M.;
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f 01-NOV-1995 (Rel. 32, Created)
T 01-NOV-1995 (Rel. 32, Last sequence upday
T 15-MAR-2004 (Rel. 43, Last annotation up
T 15-MAR-2004 (Rel. 31, Last annotation up
T 15-MAR-2004 (Rel. 33, Last annotation up
T 15-MAR-2004 (Rel. 34, Last annotation up
T 15-
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Best Local
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                                                                SEQUENCE OF 84-123 FROM N.A.
Mizrahi V., Dudding L.R.;
Submitted (MAR-1993) to the EMBL/GenBank/DDBJ
-!- FUNCTION: This enzyme is an endonuclease t
RNA-DNA hybrids specifically (By similarit
-!- CATALYTIC ACTIVITY: Endonucleolytic cleava
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AE014357;
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Matches 54
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Q985W1;
28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                         MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoti Kaneko T., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Watanabe A., Idesawa C., Kohara M., Matsumoto M., Matsuno A., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
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                                                     "Complete genome structure Mesorhizobium loti."; DNA Res. 7:331-338(2000).
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti)
Bacteria; Proteobacteria; Alphaprot
                                                                                                                                                                                                                                                                      Ribonuclease H (
RNHA OR MLR7504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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InterPro; IPR002156; RNaseH.
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EMBL; L11915; AAA25000.1;
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                                                                                                                                                                            STRAIN=MAFF303099;
                                                                                                                                                                                                                                 Phyllobacteriaceae;
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TIGR; HI0138; -.
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FUNCTION: This enzyme is an endonuclease that RNA-DNA hybrids specifically (By similarity). CATALYTIC ACTIVITY: Endonucleolytic cleavage t phosphomonoester.
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SUBCELLULAR LOCATION: Cytoplasmi
SIMILARITY: Belongs to the RNase
                                                                                                                                                                                                                  _TaxID=381;
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation updat
26.4) (RNase H)
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Pred. No. 5.6e
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METAL 10 NAGNESIUM (BY SIMILARITY).

METAL 70 YO MAGNESIUM (BY SIMILARITY).

METAL 70 YO MAGNESIUM (BY SIMILARITY).

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METAL 134 134 MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                              MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Briody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- COPACTOR: Magnesium (By similarity).
-i- SUBUNIT: Monomer (By similarity).
-i- SUBCELLULAR LOCATION: Cytoplasmic (Potentia-
-i- SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                        "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNHA OR PA1815
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phosphomonoester.
COFACTOR: Binds 1 magnesium ion per
SUBUNIT: Monomer (By similarity).
                                                                                  FUNCTION: This enzyme is an endonuclease that degrades RNA-DNA hybrids specifically (By similarity). CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
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59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.3%;
llarity 39.6%;
Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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Pred. No. 6.7e-14;
9; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
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                                 Bubunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
                              (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                   RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 11
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Best Local S
Matches 54
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Q9JTD9;
28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, I
15-MAR-2004 (Rel. 43, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                               Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher G., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Schall B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."; Nature 404:502-506 (2000).

-I- FUNCTION: This enzyme is an endonuclease that degrades the RNA RNA-DNA hybrids specifically (By similarity).
-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                        Ribonuclease HI (EC RNHA OR NMA1817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis (serogroup A)
Bacteria; Proteobacteria; Betaproteo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
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HSSP; P00647; 1RBS.
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                                                                                                                                                                                                                                                                                                            Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00075; rnaseH;
phosphomonoester.

COFACTOR: Binds 1 magnesium ion per
COFACTOR: Monomer (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 GMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHQVEWQWVRGHTGDPGNERADQLANRGVAE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALAALKRSCPIRLI--TDSEYVMRGITEWLPNWKKRGWKTASKQPVKNADLWQALDEQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVIYTDGACKGNPGRGGWGALLLYKGAERELWG-GEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVVYTDGCCSSNGRRKPRAGIGVY------WGPGHPLNVGIRLPGRQTNQRAEIHAACK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       1, Last sequence update)
3, Last annotation updat
3.1.26.4) (RNase HI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1%; Score 233.5; DB 1; 35.8%; Pred. No. 9.9e-14;
                                                                                                                                                                                                                                                                                                                              Betaproteobacteria; Neisseriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                      update)
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                       (By
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                         similarity)
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Best Local S
Matches 55
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NEIMB
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Q9JYE5;
28-FEB-2003
28-FEB-2003
                                                                                                                                                         Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Praser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup
MEDLINE=20175755; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; Betaprot
Neisseriaceae; Neisseria.
NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence updat.
15-MAR-2004 (Rel. 43, Last annotation upd.
Ribonuclease HI (EC 3.1.26.4) (RNase HI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL162757; CAB85042.1; -. 
PIR; F81807; F81807. 
HSSP; P00647; ZRN2. 
HAMAP; MF 00042; -; 1. 
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNHA OR NMB1618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                Science 287:1809-1815(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                   -1- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Nuclease;
                          FUNCTION: This enzyme is an endonuclease that degrades RNA-DNA hybrids specifically (By similarity).

CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00075; rnaseH;
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55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10710307;
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MAGNESIUM (BY SIMILARITY).

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MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 232.5; DB 1;
Pred. No. 1.2e-13;
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les 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
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                                                                                      the
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RESULT 13
RNH_ZYMMO
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Best Local
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                                                                                                                                                                                                                                                                                               RNH ZYMMO
069014;
30-MAY-2000
30-MAY-2000
28-FEB-2003
                                                                                                                SEQUENCE FROM N.A.

STRAINARICC 31821 / ZM4 / CP4;

Lee J., Jin S., Kang H.S.;

"Sequence analysis of a cosmid clone of Zymomonas mobilis containing alcohol dehydrogenase B gene.";

submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                              Zymomonas mobilis.
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Zymomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
METAL

    -!- FUNCTION: This enzyme is an endonuclease the
RNA-DNA hybrids specifically (By similarity)
    -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage

                                                                                                                                                                                                                                                                       RNHA OR RNH
                                                                                                                                                                                                                                                                                  Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; H81061; H81061.
HSSP; P00647; 2RN2.
TIGR; NMB1618; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE002512; AAF41970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                       phosphomonoester.

COPACTOR: Binds 1 magnesium ion
SUBUNIT: Monomer (By similarity)
SUBCELLULAR LOCATION: Cytoplasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: Binds 1 magnesium ion per subunit (B: SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
           SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                   TaxID=542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNQTVYLYTDGACKGN----PGAG---GWG-----VLMRYGSHEKELFGGEAQTTNNRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ-----TNQRA
                                                                                                                                                                                                                                                                                                                                                                                                                      ELDALVGRHOVSWTWVKGHAGHAENERADDLANRGAAO 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclease; Endonuclease; Magnesium; Complete;
10 10 MAGNESIUM (BY SIMILARITY)
48 48 MAGNESIUM (BY SIMILARITY)
70 70 MAGNESIUM (BY SIMILARITY)
134 134 MAGNESIUM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AA;
                                                                                                                                                                                                                                                                                (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation updat
) H (EC 3.1.26.4) (RNase H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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           Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16251 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.2%;
                         Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
           the RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 229.5; |
Pred. No. 2.2e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                    PRT;
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           H family.
                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                             update)
                         (Potential).
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                                                  subunit (By
                                                                           cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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Best Local
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Pfam; PF00075; rnaseH; 1.
Pfam; PF00075; rnaseH; 1.
Hydrolase; Nuclease; Endonuclease; Magnesium.
Hydrolase; Nuclease; Endonuclease; Magnesium (BY SIMILA 16 16 MAGNESIUM (BY SIMILA 154 54 MAGNESIUM (BY SIMILA 140 140 MAGNESIUM (BY SIMILA METAL META
                                                                                                                                                                                        Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:987-9882(2001).
-I- FUNCTION: This enzyme is an endonuclease that degrades the RNA of
RNA-NNA hybrids specifically (By similarity).
-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNHA OR RNHA1 OR R00914 OR SMC00018.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence upd 28-FEB-2003 (Rel. 41, Last annotation u Ribonuclease H (EC 3.1.26.4) (RNase H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF086791; AAC70364.1;
PIR; T33725; T33725.
HSSP; P00647; ZRN2.
HAMAP; MF_00042; -; 1.
InterPro; IRF002156; RNaseH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21396507; PubMed=11481430;
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                                                                             SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                            phosphomonoester.
COFACTOR: Binds 1 magnesium ion per subunit
                                                     SIMILARITY: Belongs to the RNase H family.
SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HDIAWKWVKGHAGHPDNERADQLASDAA 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sinorhizobium/Ensifer group; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%;
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Pred.
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No. 6.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur
Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribonuclease HI (EC RNHA OR HD1206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7VM15;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last ann
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus ducreyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: This enzyme is an endonuclease that degrades RNA-DNA hybrids specifically (By similarity). CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                               phosphomonoester.
COFACTOR: Binds 1 magnesium ion per subunit
                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                                                                                                           SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 MDIQWMHVPGHSGFIGNEEADRLAREG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 IEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3, Last sequence update)
3, Last annotation updat
3.1.26.4) (RNase HI).
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RESULT RESULT REPORT OF THE PROPERTY OF THE PR
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Pfam; PF00075;
Hydrolase; Nucl
METAL 47
METAL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21608550; PubMed-11743193;
MEDLINE-21608550; PubMed-11743193;
Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease H (EC 3.1.26.4) (RNase H).
RNHA OR ATU0776 OR AGR C 1417.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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SEQUENCE
                                             "Genome sequence of the plant pathogen a Agrobacterium tumefaciens C58."; Science 294:2323-2328 (201). "Science 194:2323-2328 (201) an endonucle RNA-DNA hybrids specifically (By sim CATALYTIC ACTIVITY: Endonucleolytic
                                                                                                                                                                                                                          MEDIINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz
Wollam C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                         Flanagan C., Crowel
Cielo C., Slater S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00042; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2317-2323(2001).
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153 AA;
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47 MAGNESIUM (BY SIY
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Pred. No. 1.2e
19; Mismatches
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  non
                                                                                                   endonuclease
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M (BY SIMILARITY).
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  subunit
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C., Mullin I
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Best Local :
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PIR; AB2672; AB2672.
PIR; H97453; H97453;
HAMAP; MF_00042; -; 1
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1
                                                                                                                                                                                                                                                                                                                                                                                             CAUCR
                                              MEDIJINE-2117398; PubMed-11259647;
Merman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson i. Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.: Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berr Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., W Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-414(2001)
                                                                                                                                                                                                                                                                                                                                  Q9A341;
28-FEB-2003
28-FEB-2003
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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METAL
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STRAIN=ATCC
                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                         Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                      Ribonuclease HI (EC RNHA OR CC3365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                        NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the RNase H family.
          RNA-DNA hybrids specifically (By similarity) CATALYTIC ACTIVITY: Endonucleolytic cleavage
                                        FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                             CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVG---IRLPGRQ---TNQRAEIHAACKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 IEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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47
69
133
146 AA;
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                                                                                                                                                                                                   19089 / CB15;
                                                                                                                                                                                                                                                                                                                    (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 43, Last annotation updat
HI (EC 3.1.26.4) (RNase HI).
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                                        This enzyme is an endonuclease that degrades
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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9 MAGNESIUM (BY SIMILARITY).
47 MAGNESIUM (BY SIMILARITY).
69 MAGNESIUM (BY SIMILARITY).
133 MAGNESIUM (BY SIMILARITY).
16261 MW; CA90796A79057155 CRC64;
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7; Mismatches
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No. 1.4
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RESULT 18
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                                                                                                              Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNH_PSESM STANDARD; PRT; 150 AA. 0877T0; 0277T0; 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Ribonuclease HI (EC 3.1.26.4) (RNase HI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DC3000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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"The complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. tomato DC3000.";
Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
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SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cycoplasmic (Potential).
SIMILARITY: Belongs to the RNase H family.
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PP000075; rnaseH; 1.

PP000006.

PP000075; rnaseH; 1.

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PP000075; rnaseH; 1.

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ro; IPR002156; RNaseH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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AC 08FP
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Best Local
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Pfam; PP00075; rnaseH; 1.
Pfam; PP00075; rnaseH; 1.
Hydrolase; Nuclease; Endonuclease; Magnesium; Complete p
METAL 10 10 MAGNESIUM (BY SIMILARITY).
METAL 48 48 MAGNESIUM (BY SIMILARITY).
METAL 70 70 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
METAL 134 MAGNESIUM (BY SIMILARITY).
                                                                                 SEQUENCE FROM N.A.

MEDLINB=22423060; PubMed=12534463;

Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Holmes i

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes i

Brinkac L., Beanan M., DeBoy R.T.; Daugherty S., Kolonay J.,

Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,

Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,

Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,

Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last ann
15-MAR-2004 (Rel. 43, Last ann
Ribonuclease HI (EC 3.1.26.4)
RNHA OR PP4142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>'</del>
"Complete genome sequence and comparative analysis of metabolically versatile Pseudomonas putida KT2440.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q88FF5;
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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InterPro; IPR002156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida (strain KT2440)
                                                            Fraser C.M.;
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SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the RNase H
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3, Last sequence update)
3, Last annotation updat
3.1.26.4) (RNase HI).
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Pred. No. 1.7e-12;
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Best Local S
Matches 54
SEQUENCE FROM N.A.

STRAIN=ATCC 33913 / NCPPB 528;

MEDLINE=2002145; PubMed=12024217;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Katsuyama A.M., Kishi L.T., Madeira A.M.B.N., Martinez-Rossi N.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNH XANCP
Q8PBX8;
                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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phosphomonester.

COFACTOR: Binds 1 magnesium ion per

SUBUNIT: Monomer (By similarity).

SUBUNIT: MONOMER (Cytoplasmic

SUBULLIULAR LOCATION: Cytoplasmic
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CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the RNase H
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lase; Nuclease; E
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ro; IPR002156; RNaseH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (Rel. 41, Created)
3 (Rel. 41, Last sequ
3 (Rel. 41, Last anno
5 (EC 3.1.26.4) (R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e; Endonuclease; Magnesium; Complete;
10 MAGNESIUM (BY SIMILARITY).
48 MAGNESIUM (BY SIMILARITY).
70 MAGNESIUM (BY SIMILARITY).
134 MAGNESIUM (BY SIMILARITY).
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st annotation
5.4) (RNase H)
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Pred. No. 2.1
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Best Local S
Matches 55
                                                                                                                                                                                                                RNH RALSO STANDARD; PRT; 1
Q8XZ91;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Ribonuclease H (EC 3.1.26.4) (RNase H)
RNHA OR RSC1513 OR RS03791.
                                                                                                                                                                                                                                                                                                                                                                             ULT 21
_RALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.ishorsend an email to license agreement (See http://www.ishorsend.agreement (See http://www.ishorsend.agreement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martins B.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H. Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with dinost specificities.";
MEDLINE=21681879; PubMed=11823852; Salanoubat M., Genin S., Artiguena Arlat M., Billault A., Brottier P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           host specificities.;
Nature 417:459-463(2002).
-i- FUNCTION: This enzyme is an
                                                                STRAIN=GMI1000;
                                                                                                                                                    Bacteria; Proteobacteria;
Burkholderiaceae; Ralstoni
                                                                                                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria: Betaproteobacteria: Burk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send
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COFACTOR: Binds 1 magnesium ion per subunit (B) SUBUNIT: Monomer (By similarity)

SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytop SIMILARITY: Belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-DNA hybrids specifically (By sin CATALYTIC ACTIVITY: Endonucleolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHAATQRHS I EWRWVKGHNGDPDNERVDVLARNQA
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69
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                                                                                    N.A.
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69
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9 MAGNESIUM (BY SIMILARITY).
47 MAGNESIUM (BY SIMILARITY).
69 MAGNESIUM (BY SIMILARITY).
33 MAGNESIUM (BY SIMILARITY).
16743 MW; DE84CDFB07D0B172 CRC64;
S., Artiguenave
., Brottier P., (
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t annotation u
.4) (RNase H).
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y (By similarity).
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Gouzy J
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                                                                                                                                                                             Burkholderiales;
J., Mangenot S
, Cattolico L.,
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Oliveira V.R.,
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Best Local (
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METAL 9 9 MAGNESIUM (BY SIMILARITY).

METAL 47 47 MAGNESIUM (BY SIMILARITY).

METAL 69 69 MAGNESIUM (BY SIMILARITY).

METAL 133 133 MAGNESIUM (BY SIMILARITY).

SEQUENCE 151 AA; 16598 MW; A64CDD79C7F98143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphomonoester.
-!- COPACTOR: Magnesium (By similarity).
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the plant pathogen Ralstonia Nature 415:497-502(2002).
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Siguier P., Thebault P., W
Weissenbach J., Boucher C.
               SEQUENCE OF 44-110
STRAIN=LR222;
                                                       STRAIN=LR222;
Dawes S.S., Crouch R.
Submitted (JAN-1995)
                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00042; -; 1.
InterPro; IPR002156; RNaseH.
                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL646065; CAD15215.1; -.
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MEDLINE=94124016; PubMed=8294019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: This enzyme is an endonuclease that degrades the RNA RNA-DNA hybrids specifically (By similarity).
CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                                                                                                                                                          111
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                              FROM
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                                                        the
                                                                     Morris S.L.,
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                                                          EMBL/GenBank/DDBJ
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Pred. No. 3.3e-12;
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                                                                      Mizrahi
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                                                          databases
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RESULT 23
RNH YERPE
ID - RNH YERPE
ID - RNH 28-FE
DT 28-FE
DT 15-MA
DE Ribon
GN Yersi
OC Enter
OC Enter
OC NCBI
RN | [1]
RN | [1]
RN | [1]
RN | [1]
RP SEQUE
RA Baker
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Pfam; PF00075; rnaseH; 1.
Pfdm; PF00075; rnaseH; 1.
Hydrolase; Nuclease; Endonuclease; Magnesium.
Hydrolase; Nuclease; Endonuclease; Magnesium.
HMETAL 11 11 MAGNESIUM (BY SIMI.
METAL 72 72 MAGNESIUM (BY SIMI.
METAL 136 136 MAGNESIUM (BY SIMI.
METAL 14 MAGNESIUM (BY SIMI.
METAL 15 MAGNESIUM (BY SIMI.
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Best Local
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CONFLICT
SEQUENCE
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"A PCR method for the sequence analysis of the gyrA, polA a
gene segments from mycobacteria.";
Gene 136:287-290(1993).
-i- FUNCTION: This enzyme is an endonuclease that degrades
RNA-DNA hybrids specifically.
-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
STRAIN=CO-92 / Biovar Orientalis; MEDLINE=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., Titb Prentice M.B., Sebaihia M., James K.D., Ch Baker S., Basham D., Bentley S.D., Brooks Chillingworth T., Cronin A., Davies R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            RNH YERPE STANDARD; PRT; 154 AA. Q8ZH30; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Ribonuclease HI (EC 3.1.26.4) (RNase HI). RNHA OR YPO1081 OR Y3095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U20115; AAA62124.1; -. HSSP; P00647; IGOA. HAMAP, MF_00042; -; 1. InterPro; IPR002156; RNABeH.
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                                                                                                                                                                                                                                                                                                                                                                          Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Yersinia.
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COPACTOR: Binds I magnesium ion per subunit (By SUBUNIT: Monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Potential).

SIMILARITY: Belongs to the RNase H family.
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Pred. No. 3
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   Titball R.W., Holden M.T.., Churcher C., Mungall K.ooks K., Cerdeno-Tarraga A.M., Davis P., Dougan G.,
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DT 28
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DE R1
GN RN
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COS V1
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Best Local S
Matches 55
(Rel. 41, Created)
T 28-FBB-2003 (Rel. 41, Last sequence upd.
T 15-MAR-2004 (Rel. 43, Last annotation up.
Ribonuclease HI (EC 3.1.26.4) (RNase HT)
RNHA OR VC2234.
Vibrio cholere
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VIBCH
RNH_VIBCH
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STRAIN-KIM5 / Biovar Mediaevalis;
STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Ma:
Deng W., Burland V., Mau B., Zhou S., Schwartz D.:
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.:
Petherston J.D., Lindler L.E., Brubaker R.R., Plano
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano
Straley S.C., McDonough K.A., Nilles M.L., Matson J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perry R.D.;
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-I- FUNCTION: This enzyme is an endonuclease that de RNA-DNA hybrids specifically (By similarity).
-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to
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COFACTOR: Binds 1 magnesium ion per subunit
SUBUNIT: Monomer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Potenti:
SIMILARITY: Belongs to the RNase H family.
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                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 HAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00075; rnaseH; 1.
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ro; IPR002156; RNaseH.
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Moule S., Oyston F
, Skelton J., Steve
uence of Yersinia p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.9%;
llarity 35.7%;
Conservative 1
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S., Oyston P.C.F., (
on J., Stevens K., V
f Yersinia pestis, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CEVTLSTDSQYVRQGITQWIHNWKKRGWKTADRKPVRNVDLWQRL
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Pred. No. 5e-12;
6; Mismatches
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, Quail M.A., Rutherford K.,
, Whitehead S., Barrell B.G.
, the causative agent of pla
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tson J.S., Blattner
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BARRAB

RNH VIBVU Q8DBD5; 10-OCT-2003 ( 10-OCT-2003 ( 15-MAR-2004 ( Ribonuclease

STANDARD;

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(Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 43, Last annotation updat
HI (EC 3.1.26.4) (RNase HI).

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Matches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M. Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D. Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Selle McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter
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STRAIN=E1 Tor N16961 / Serotype O1;
MEDLINE=20406833, PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clay
Dodson R.J., Haft D.H., Hickey E.K., Peterson
Gill S.R., Nelson K.E., Read T.D., Tettelin H.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; VC2234; -. 1.
HAMAP; MF 00042; -; 1.
InterPro; IPR002156; RNASeH.
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Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00647; 2RN2.
TIGR; VC2234; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the RNase H family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: This enzyme is an endonuclease that RNA-DNA hybrids specifically (By similarity). CATALYTIC ACTIVITY: Endonucleolytic cleavage t
                                                                                                                                                                                                                                                                       136 MGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPG-----HPLNVGIRLPGRQTNQ
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                                                                                                                                                       RAEIHAACKAIEQAĶTQNINKLVĻYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKED
                                                                                                                                                                                                                  MNKQVEIFTDGSCLGNP-----GPGGYGIVMRYKQVEKTLARGYRL---TTNN
WQALDKETARHQVEWRWVKGHAGHRENEMCDELARQAAENPTED
                                               FVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ-SED
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134 1
156 AA;
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17953 MW;
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                                                                                                          -CRVILTIDSQYVRQGITQWIHNWKLRGWKTADKKPVKNADL
                                                                                                                                                                                                                                                                                                                         Score 214; DB
Pred. No. 5.6e
21; Mismatches
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MAGNESIUM
MAGNESIUM
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ESIUM (BY SIMILARITY).
ESIUM (BY SIMILARITY).
ESIUM (BY SIMILARITY).
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Sellers P.,
White O.,
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                                                                                                             103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Nuclease; Endonuclease; Magnesium; Complete proteome.
METAL 10 10 MAGNESIUM (BY SIMILARITY).
METAL 48 48 MAGNESIUM (BY SIMILARITY).
METAL 70 70 MAGNESIUM (BY SIMILARITY).
METAL 134 134 MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CMCP6;
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HAMAP; MF_00042; -; 1.
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Vibrionaceae; Vibrio.
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Pfam; PF00075;
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                                                  117 DWRWYKGHAGHRENEMCDELARAAAE 142
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                                                                             QWMHVPGHSGFIGNEEADRLAREGAK 282
                                                                                                    ALKEPCN-VILTIDSQYVRQGITQWIHNWKKRGWKTADKKPVKNADLWQALDKETTRHTI 116
                                                                                                                                                             VEIFTDGSCLGN---PGPGGYGVVLRYKQVEKTLAQGYRL--
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_IPR002156; RNaseH.
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155 AA;
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            7,
            2004, 08:05:41
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                                                                                                                                                                                                                                                                       E0F8F026F87EC079 CRC64;
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Maximum DB
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Perfect score:
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Maximum Match 100%
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C:Species: Drosophila melanogaster
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 17-Nov-2000
C;Accession: JC5787
R;Filippov, V.; Filippova, M.; Gill, S.S.
Biochem. Biophys. Res. Commun. 240, 844-849, 1997
A;Title: Functional characterization of RNase H1 from Drosophila melanogaster.
A;Reference number: JC5787; MUID:98063328; PMID:9398656
A;Accession: JC5787; MUID:98063328; PMID:9398656
A;Accession: JC5787
A;Molecule type: DNA
A;Residues: 1-333 <FIL>
A;Ccomment: This enzyme degrades the RNA molecular in a RNA:DNA hydrid.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F5
A;Reference number: Z18526
A;Recession: T15506
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-369 <NHA>
A;Residues: 1-369 <NHA>
C;Genetics:
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A; Introns:
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                                                                   ;Cross-references: FlyBase:FBgn0023171;Introns: 104/2; 123/1; 202/1; 292/1
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Best Local Similarity
Matches 108; Conserv
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Gene: CESP:F59A6.6
                     Query Match
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      Local Similarity
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%; Pred. No. 2.7e-31;
44; Mismatches 103; Indels 105;
      Score 422; DB 2;
Pred. No. 1e-29;
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A; Introns: 23/2
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-264 <BOR>
A;Cross-references: EMBL:AL121815; PIDN:CAB58158.1; GSPDB:GN00067; SPDB:SPBC336.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: T40244
R;Borzym, K.; Beck, A.; Reinhardt, R.; McDougall, R.C.; Rajandream, submitted to the EMBL Data Library, October 1999
A;Reference number: Z21916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribonuclease h1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                           122 VEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPG-RQ
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                                                                                                                                                             TNORABIHAACKAIBQAKTONINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
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LDLINRASDLMSDRNVSLEYVKGHSTDYGNQQADMLARRGASE
                                             KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
                                                                                                          TNNRAELQAIILALENTS----GDLTIRSDSNYSIKSLTTWLPKWKKNDFKTSNSQPVKN
                                                                                                                                                                                                                                                                                                                                 STTSYGYSPYSSSSSNYSARHSDKYRKKISRSYSTEKDIEIFSNDTHEKS-----
                                                                                                                                                                                                                                                                                                                                                                                  -----KSASPEVSEGHENQHGQE-SEAKPGKRLREPLDGDGHESAQPYAKHMKPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 323.5; DB 2; 
; Pred. No. 4.3e-21; 
41; Mismatches 105;
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B.G.

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ribonuclease H1 homolog (EC 3.1.-.-) -
C;Species: Crithidia fasciculata
C;Jate: 07-Apr-1994 #sequence_revision
C;Accession: A48683
                                                                                                                                                                                                                                                                                 R;Campbell, A.G.; Ray, D.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 9350-9354, 1993
A;Title: Functional complementation of an Escherichia coli ribonuclease H mutation A;Reference number: A48683; MUID:94022373; PMID:8415705
A;Accession: A48683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL;AF048992; PIDN:AAC04366.1
A;Experimental source: Strain 912
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1998
A;Description: Genomic and cDNA sequences of Schizosaccharomyces pombe Ribonuclease
A;Reference number: Z22591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribonuclease H1 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces nombe
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A;Introns: 23/2
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A;Molecule type: DNA
A;Residues: 1-264 <TOZ>
A;Cross-references: EMBL:AF048992;
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                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                  ;Molecule type: DNA
;Residues: 1-494 <CAM>
                                                                                                                                 Matches
                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                  Keywords: hydrolase
                                                                                                                                                                                                                  Cross-references: GB:L18916; NID:g5776548; PIDN:AAA03546.1; PID:g310977
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                               FVRKSASPEVSEGHENOHGOE-----SEAKPGKRLREPLDGDG----HESAQPYAKHM 118
                                                                                              RVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDLINRASDLMSDRNVSLEYVKGHSTDYGNQQADMLARRGASE 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPG-RQ
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YL--TAHPARSGLEKSDRGDGAASLSALSEPQVGLRRSRAAEAEASYVVEAPAQPTLRQR
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ilarity 29.3%;
Conservative` '
                                                                                                                                Conservative
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                                                                ·ASRMKPSFYVVAVGRQRGIYSTWDQCSEQVKGFSGAVYKSFRTLSEARA
                                                                                                                                                19.4%;
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Pred. No. 9.6e-21;
2; Mismatches 105;
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                                                                                                                                                 Score 299.5; DB 2;
Pred. No. 1.2e-18;
                                                                                                                                Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                   Crithidia fasciculata
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                                                                                                                                                               Length 494;
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RESULT
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A;Restdues: 1-348 <5KE>
A;Restdues: 1-348 <5KE>
A;Restdues: 1-348 <5KE>
A;Cross-references: EMBL:Z49939; NID:g887599; PID:g887615; MIPS:YMR234w
A;Experimental source: strain AB972
R;Itaya, M.; McKelvin, D.; Chatterjie, S.K.; Crouch, R.J.
Mol. Gen. Genet. 227, 438-445, 1991
A;Title: Selective cloning of genes encoding RNase H from Salmonella type
A;Reference number: S16816; MUID:91326035; PMID:1650910
A;Accession: S16816.
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C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 183-348 <ITA>
A;Cross-references: EMBL:X57160
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N;Alternate names: protein YM9959.16; protein YMR234w
뭉
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A;Accession: S57601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: $57601; $16816
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Best Local :
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296
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LVQRFVKVKKYYELNKECF----KNNGKFQIEW--VKGHDGDPGNEMADFLAKKGASR
                                                                                                                                                                                                                VSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVG-IRLPGRQTNQRAE 186
                                                                                                                                                                                                                                                                                                                                                                                             ASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPSVEP--APPVSRDTFSYMGDFVVVYYTDGCCSSNGRRKPRAGIGVYWG---PGHPLNVG 173
                                                                                                                                                                                                                                                                                                           -----QPYAKH----
                                                                                                                                                                                                                                                                                                                                                  AGGOVSKPHTTO-----KRVHRRNRPLHYSSLTSSACSSLSSANTNTFYSVKSNVPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERL-----
                                                                                      I EAVSEALKKIWEKLTNEKEKVNYQIKTDSEYVTKLLNDRYMTYDNKKLEGLPNSDLIVP
                                                                                                                             IHAACKAIEQ--AKTONINKLVLY---TDSMFTINGITNWVQGWKKNGWKTSAGKEVI--
                                                                                                                                                                         LSSNTM--YNKSMNVYCDGSSFGNGTSSSRAGYGAYFEGAPEENISEPLLSGAQTNNRAE
                                                                                                                                                                                                                                                             IESKI FNNWKDCQAYVKHKRGITFKKFEDQLAAENFISGMSAHDYKLMNISKESFESKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDSRYVIDGLTRYALKWVANGFKLASKEPVLNQDLWRQLIRLRDAYNTRYAEQQHWAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Churcher, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD:S0004847; MIPS:YMR234w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 249.5; DB 2
26.0%; Pred. No. 2.2e-14;
tive 38; Mismatches 112
                                      NKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         June 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhimurium,
                                                                                                                                                                                                                                                                                                           ----MKPSVEPAPP
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  347
                                                                                      295
                                                                                                                                                                                                                                                                177
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                                                                                                                                239
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                                                                                                                                                                                                                                                                                                                                                                                                111
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A;Molecule type: DNA,
A;Residues: 1-154 <KUR>
A;Residues: 1-154 <KUR>
A;Cross - references: GB.AE008917; PIDN:AAL52638.1; PID:g17983460; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
C;Genetics:
A;Gene: BMEI1457
A;Map position: I
C;Superfamily: ribonuclease H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calf thymus ribonuclease H (EC 3.1.26.4) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Pate: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002 C;Accession: AC3434 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Golteman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-169 <COL>
A;Cross-references: GB:AE001215; GB:AE000520; NID:g3322631; PIDN:AAC65340.1; PID:g33226:
A;Experimental source: strain Nichols
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                           8
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AC3434
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C;Superfamily: ribonuclease H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: G71333
A;Status: preliminary; nucleic acid sequence not shown;
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Best Local S
Matches 52
                                                                                                                                                                                    Matches
                                                                                                                                                                                                         Query Match
Best Local Similarity
190 ACKAIEQAKTQNINKLVLYIDSMFTINGITNWVQGWKXNGWKTSAGKEVINKEDFVALER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 NKDLWEALSALADALSVEWRWVKGHAGDPYNELCDRLATDAARRA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 NKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQS 284
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                                                                                                                             140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ------TNQRAEIHA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 QTNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVI
                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 LTLYTDGACLGNPGPGGWAFALVPSDVPFLETGQXAPEAAAFTRSGSAYP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
52; Conserv
                                                                              IEAYTDGACSGN----PGPG---GWG-----ALLRWNGNEKELKGGEAETTNNRMELMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STNNRMELCAVINALQEAHGRAAEAVVVVVTDSQYVRKGITQWIHTWKHNGWKTAAKQPVK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.5%;
ilarity 31.5%;
Conservative 2
                                                                                                                                                                               Conservative
                                                                                                                                                                            15.4%; Score 238.5; DB 2; Length 154; .37.1%; Pred. No. 7.6e-14; ltive 21; Mismatches 49; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 239; DB 2; Length 169; pred. No. 7.7e-14; 25; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation
                                                                                                                                                                               25;
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                            249
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McDd
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ribonuclease H (EC 3.1.26.4) - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 21-Jul-2000
C;Accession: C64050
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-302 «KUR»
A;Residues: 1-302 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB77666.1; PID:g17135120; GSPDB:GN00179
A;Experimental source: strain PCC 7120
A;Experimental source: strain PCC 7120
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF1824
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
AF1824
ribonuclease H [imported] - Nostoc
                                                                                                                                                                                                                                                               A;Cross-references: GB:U32699; GB:L42023; NID:g3212180; PIDN:AAC21809.1; PID:g1573091; C;Superfamily: ribonuclease H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                    C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                             A;Residues: 1-154 <TIGR>
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic
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                                                                                                                                       Query Match
Best Local Similarity
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                                                          140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 ---QAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 GMDIQWMHVPGHSGFIGNEEADRLAR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 VYTDGCCSSNGRRKPRA---GIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 ARKAHKVTWHWIKGHAGHPENERADELARAG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 DSGQAE----PITLYTDSEYLINCVTKWVKGWKKKKGWKKKSDGNPVQNQDLLETLDEL-N 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 IYTDGACTGN----PGPGGWGVVVYFSDGSVHEMG-DAAKHTTNNKMEMQAAIAALKFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
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57; Conserv
   v
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IEIFTDGSCLGN----PGAG-
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                  acid sequence not shown; translation not shown
                                                                                                                                          15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.4%; Score 238; DB 2; 39.0%; Pred. No. 1.9e-13;
                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                          Score 236.5; DB 2
Pred. No. 1.1e-13;
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GIGAVLRYKQHEKTLSKGYFQTTNNRMEL
                                                                                                                  49;
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                                                                                                                  Indels
                                                                                                                                                                         Length
                                                    -----TNORAEI 187
                                                                                                                     29;
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09-Dec-2002
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                                                                                                                  Gape
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ribonuclease H (EC 3.1.26.4) I NMA1817 [imported] - Neisseria meningitidis (strain Z2491 C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: F81807 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: F81807
                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-145 < PAR>
A; Cross-references: GB: AL162757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-148 <STO>
A;Cross-references: GB:AE004608; GB:AE004091; NID:g9947797; PIDN:AAG05204.1; GSPDB:GN001
A:Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, i Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                       A;Gene: rnhA; NMA1817
C;Superfamily: ribonuclease
C;Keywords: hydrolase
                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                                                                         A; Status: preliminary
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C;Superfamily: ribon
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Query Match
Best Local Similarity
                                                                                                                                              Genetics:
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Best Local (
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Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 VVVYTDGCCSSNGRRKPRAGIGVY------WGPGHPLNVGIRLPGRQTNQRAEIHAACK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVAL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIEQAKTQNINKLVLYTDSMETINGITNWVQGWKKNGWKTSAGKEVINKEDEVALERLTQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESIGRHKINWOWVKGHAGHRENEICDELAKKGAE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVIYTDGACKGNPGRGGWGALLLYKGAERELWG-GEP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHQVEWQWVRGHTGDPGNERADQLANRGVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALAALKRSCPIRLI--TDSEYVMRGITEWLPNWKKRGWKTASKQPVKNADLWQALDEQVA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribonuclease H
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                                                                                                                                                               serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1%; Score 233.5; DB 2; 35.8%; Pred. No. 2e-13;
15.0%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                               GB:AL157959; NID:g7380371; PIDN:CAB85042.1; PID:g73804 A, strain Z2491
    Score
Pred.
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  232.5; DB 2;
No. 2.4e-13;
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                      Length 145;
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C; Genetics:
A; Gene: rnh
C; Function:
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A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.;
                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribonuclease HI NMB1618 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: H81061
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                                                                                                                                                R;Lee, J.S.; Jin, S.J.; Kang, H.L.; Kang, H.S. submitted to the EMBL Data Library, August 1998 A;Description: Sequence analysis of 67E10 cosmid A;Reference number: 221392
                                                                                                                                                                                                                                                                                 ribonuclease H (EC 3.1.26.4) - Zymomonas mobilis C;Species: Zymomonas mobilis C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999
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C;Superfamily: ribonuclease
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                                                                   A;Cross-references:
                                                                                     A; Molecule type: DNA
A; Residues: 1-156 < LEE>
                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                              C; Accession: T33725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
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                                                                                                                                                                                                                                                                                                                                                                                                                                          BLDALVGRHQVSWTWVKGHAGHAENERADDLANRGAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALERLTOGMDIOWMHVPGHSGFIGNEEADRLAREGAKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIHAACKAIEQAKTONINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNQTVYLYTDGACKGN----PGAG----GWG-----VLMRYGSHEKELFGGEAQTTNNRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ-----TNQRA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELDALVGRHOVSWTWVKGHAGHAENERADDLANRGAAO 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNQTVYLYTDGACKGN----PGAG---GWG----VLMRYGSHEKELFGGEAQTTNNRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELTÄVIEGLKSLKRR--CTVIICTDSQYVKNGMENWIHGWKRNGWKTASKQPVKNDDLWK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELTAVIEGLKSLKRR--CTVIICTDSQYVKNGMENWIHGWKRNGWKTAAKQPVKNDDLWK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%;
ilarity 34.2%;
Conservative 2
                                                                 EMBL:AF086791; NID:g3820581; PID:g3089615; PIDN:AAC70364.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 229.5; DB 2
Pred. No. 4.5e-13;
3; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB2672
A;Accession: AB2672
A;Catus: preliminary
A;Moleule type: DNA
A;Residues: 1-146 < KUR>
A;Residues: 1-146 < KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41792.1; PID:g17739146; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0776
A;Map position: circular chromosome
C;Superfamily: ribonuclease H
                     ribonuclease H (EC 3.1.26.4) mutant with his 62 rep C;Species: Agrobacterium tumefaciens C;Date 30.5ep-2001 #sequence_revision 30.5ep-2001 C;Accession: H97453 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; R;Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D. Science 294, 2323-2328, 2001
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H97453
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    A;Title:
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1 Similarity 37.8%;
56; Conservative 2
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; Pred. No. 1.4e-12;
21; Mismatches 54;
      Plant
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Pred. No. 2.8e-12;
Pred. No. 54;
                                         S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
  Pathogen
    and
                                                                                                                                                replaced by
                                                                                                       #text_change 18-Nov-2002
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Markelz,
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calf thymus ribonuclease H (EC 3.1.26.4) [imported] C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 C;Accession: AI01132 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball,
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AI0132
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[imported]

Yersinia pestis

(strain

#text\_change 27-Nov-2001

R. ₩. ;

Holden,

3 H

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Prentice,

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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolong n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87666
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C;Superfamily:
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A; Cross-references: GB:
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A; Residues: 1-146 < KUR>
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                                                                                                                                                                                                                                                                   Similarity
                               LTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQS
                                                                                                     AIEQAKTQNINK---LVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALER
                                                                                ALEL-----LNRPCVVELHTDSQYVMKGIQEWIRGWKARGWKTADKSPVKNDDLWKRLDA 109
                                                                                                                                                              VTIYTDGACKGN----PGPG-----GWGAILFYGDKKKEICGGEPG-TTNNRMELMAAIQ
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ARARHDVDWRWVKGHAGHPLNERADALANEGLRQA
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                                                                                                                                                                                                                                                                                                                            ribonuclease
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llarity 36.1%;
Conservative 2:
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40.1%; Pred. No. 2.8e-12;
vative 17; Mismatches 54
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Pred. No. 3.5e-12;
1; Mismatches 53;
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A;Residues: 1-156 <HEI>
A;Cross-references: GB:AE004295; GB:AE003852; NID:g9656789; PIDN:AAF95378.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
RESULT
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C; Superfamily: ribonuclease H
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A;Accession: G82101
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Nature 406, 477-483, 2000
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: G82101
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A; Residues: 1-154 < KUR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AL590842;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                    20
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                             136
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                                                                                                                                                                                                                   184 RAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKED 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 HAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVAL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ-----TNQRAEI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
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                                                                                                                                                                                                                                                                                                           MGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPG------HPLNVGIRLPGRQTNQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAAIVALEALTSP--CEVTLSTDSQYVRQGITQWIHNWKKRGWKTADRKPVRNVDLWQRL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEIFTDGSCLGNP-----
                                                                                     WOALDKETARHOVEWRWVKGHAGHRENEMCDELARQAAENPTED
                                                                                                                           FVALERLTQGMDIQWMHVPGHSGFIGNBEADRLAREGAKQ-SED 286
                                                                                                                                                                                                                                                                 MNKQVEIFTDGSCLGNP------GPGGYGIVMRYKQVEKTLARGYRL---TTNN
                                                                                                                                                                         RMEMLAAVMALQALKEP--CRVILTTDSQYVRQGITQWIHNWKLRGWKTADKKPVKNADL 103
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                                                                                                                                                                                                                                                                                                                                                     Score 214; DB 2;
Pred. No. 1.2e-11;
21; Mismatches 57
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Pred. No. 1e-11;
6; Mismatches 54;
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R;Kanaya, S.; Crouch, R.J.
J. Biol. Chem. 258, 1276-1281, 1983
A;Title: DNA sequence of the gene coding for Escherichia A;Reference number: A92401; MUID:83108846; PMID:6296074
A;Accession: A92401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-155 COX>
A;Cross references: GB:KO4027; NID:g42061; PIDN:CAA27660.1; A;Cross references: GB:KO4027; NID:g42061; PIDN:CAA27660.1; B;KANAYA, S.; Crouch, R.J.
J. Bacteriol. 154, 1021-1026, 1983
J. Bacteriol. 154, 1021-1026, 1983
J. Title: Low levels of RNase H activity in Escherichia coli A;Reference number: I54847; MUID:83185998; PMID:6302075
A;Accession: I54847
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C;Species: Escherichia coli
C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 01-Mar-2002
C;Accession: A92401; A93979; S13170; B24257; I54847; H64745; A00793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1.155 < RES>
A;Cross-references: EMBL:V00337; NID:g42776; PIDN:CAA23620.1;
A;Cross-references: EMBL:V00337; NID:g42776; PIDN:CAA23620.1;
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
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7. Mol. Biol. 190, 113-117, 1986
A;Title: DNA sequence and coding properties of mutD(dnaQ)
A;Reference number: A24257; MUID:87060973; PMID:3023634
A;Accession: B24257
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A;Title: Role of cysteine residues in ribonuclease H from
A;Reference number: S13170; MUID:91024947; PMID:2171503
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A;Cross-references: GS:K00552; GB:J01676; GB:V00337; NID:g147676; A;Cross-references: GS:K00552; GB:J01676; GB:V00337; NID:g147676; R;Maki, H., Horiuchi, T.; Sekiguchi, M.
Proc. Natl. Acad. Sci. U.S.A. 80, 7137-7141, 1983
A;Title: Structure and expression of the dnaQ mutator and the RNat A;Reference number: A33979; MUID:84070781; PMID:6316347
A;Recession: A93979
                                                                                                                                                                                                                          C; Superfamily: ribonu
C; Keywords: hydrolase
                                                                                                                                                                                                                                                  A, Description: an endonulease that degrades the RNA of C, Superfamily: ribonuclease H \,
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A;Map position: 5 min
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A;Cross-references: GB:K00985; GB:M30201; NID:g147678; PIDN:AAA24565.1; PID:g147680
R:Kanaya, S.; Kimura, S.; Katsuda, C.; Ikehara, M.
                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000130; GB:U00096; NID:g1786402; A;Experimental source: strain K-12, substrain MG1655
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                                                                                                        Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: nucleic acid sequence not shown; translation not shown
                                                     140
                                                                                                                                         Similarity
                                                  VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKT 199
VEIFTDGSCLGNPGPGGYGAILRYRGREKTFSAGYT---RTTNNRMELMAAIVALEALKE 61
                                                                                                              Conservative
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                                                                                                           Score 208.5;
Pred. No. 3.5e
16; Mismatches
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Burland, V.;
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QNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQWM 259

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                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C;Accesion: B90655
C;Accesion: B90655
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, DNA Res. B, 11-22, 2001
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-155 <HAY>
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C;Superfamily: :
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Best Local Similarity
Matches 52; Conserv
                                                                                                 Query Match
Best Local
                                        140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKT 199
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                                                                                                   Similarity
         VEIFTDGSCLGNPGPGGYGAILRYRGREKTFSAGYT--
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                                                                                                 13.5%;
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                                                                             Score 208.5; DB 2;
Pred. No. 3.5e-11;
6; Mismatches 69;
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         -RTTNNRMELMAAIVALEALKE 61
                                                                                                                  Length
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                                                                               Gaps
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K.; Apodaca
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RESULT 23
S21659
ribonuclease H (EC 3.1.26.4) - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S21559
                                                                                                                                                                                                                                                                                                                                                                          , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribonuclease H [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT] C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AE0534 C;Accession: AE0534 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-155 <ITA>
A;Residues: 1-155 <ITA>
A;Cross-references: EMBL:X57159; NID:g48821; PIDN:CAA40447.1; PID:g48822
C;Superfamily: ribonuclease H
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Itaya, M.; McKelvin, D.; Chatterjie, S.K.; Crosubmitted to the EMBL Data Library, January 1991 A;Reference number: S21659
A;Accession: S21659
                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-155 < PAR>
                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                               A; Cross-references:
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                                                                                                                                                                            Superfamily:
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                                                                                               Local
140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKT 199
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                                                              Similarity
52; Conserv
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                                                           13.4%;
nilarity 36.6%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                              Score 206.5; DB 2
Pred. No. 5.3e-11;
6; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 206.5; DB 2
Pred. No. 5.3e-11;
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                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                               PID:g16501540; GSPDB:GN00176
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VEIFTDGSCLGNPGPGGYGAILRYRGHEKTFSEGYTL--

-TTNNRMELMAAIVALEALKE

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A;Cross-references: GB:AE004030; GB:AE003849; NID:g9107292; PIDN:AAF84957.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.B.; Kuramae, E.B.; Lalgu
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.G. de Oliveira, R.C.; Palmieri,
A;Authors: L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Silva, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
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Search completed: October Job time : 45 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: XF2158
C;Superfamily: ribonuclease H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Accession: F82591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer
Nature 406, 151-157, 2000
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C;Species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Contents: annotation
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Best Local S
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                                                                                                                                                                                                                                                                                            IEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQG 253
                                                                                                                                                                                                                                               LE--RLSEPCQIKLHTDSQYVRQGITEWMSGWVRRGWKTAAGDPVKNRDLWERLCAATQR 115
                                                                                                                                                                                                                                                                                                                                                                     YTDGSCLGNP------GPGGWAVLLRYKNNEKELVGGELDTTNNRMELMAAIMA
                                                                                                                                                                                                                                                                                                                                                                                                                               YTDGCCSSNGRRKPRAGIGVYWGPG-----HPLNVGIRLPGRQ---TNQRAEIHAACKA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.6%; Score 194.5; DB 2; llarity 35.2%; Pred. No. 6e-10; Conservative 17; Mismatches 54;
                            7, 2004, 08:09:10
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Result
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                       1546
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1086.5
1085.5
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1045.5
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1: "/Ggn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
2: /Ggn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
3: /Ggn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
4: /Ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /Ggn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
6: /Ggn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
6: /Ggn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
7: /Ggn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /Ggn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10: /Ggn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /Ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /Ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
13: /Ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
14: /Ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /Ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: /Ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
17: /Ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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1546
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APPLICANT: Crooke, Stanley T.

APPLICANT: Lima, Walter F.

APPLICANT: Lima, Walter F.

APPLICANT: Lima, Walter F.

APPLICANT: Wu, Hongjiang

ITITLE OF INVENTION: Human RNase H Compositions and Uses Thereof

FILE REFERENCE: ISPH-033

CURRENT APPLICATION NUMBER: US/09/861,205

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: 09/203,716

PRIOR APPLICATION NUMBER: 09/203,716

PRIOR PILING DATE: 1998-12-02

INUMBER OF SEG ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEG ID NO 1

LENGTH: 286

TYPE: PRT

ORGANISM: Homo sapiens
; Sequence 1, Application US/10054313
; Publication No. US20020110892A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter F.
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human RNase H Co
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Matches 286; Conserv
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Patent No. US20020076712A1
GENERAL INFORMATION:
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US-10-437-963-160683
US-10-437-963-193694
US-10-437-963-133329
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CURRENT APPLICATION NUMBER: US/10/358,439
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/861,205
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-08
PRIOR FILING DATE: 2000-10-06
PRIOR PRILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/343,809
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
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CURRENT PILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 286
 Best Loca
Matches
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PRIOR FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 286
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Publication No. US20030144496A1
GENERAL INFORMATION:
                  Query Match
Best Local :
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APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H and Compositions
FILE REFERENCE: ISPH0725
FILE REFERENCE: ISPH0725
                                                                                       LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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                 100.0%;
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Score 1546; DB 14;
Pred. No. 8.8e-152;
Mismatches 0;
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   Indels
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FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT ETLING DATE: 2003-05-28
PRIOR PELLING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR PILLING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,917
PRIOR PILLING DATE: 2001-10-09
PRIOR FILLING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILLING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILLING DATE: 2002-10-09
PRIOR FILLING DATE: 2002-10-09
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APPLICANT:
APPLICANT:
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APPLICANT:
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                       DR FILING DATE: 2002-05-17
DR FILING DATE: 2002-10-09
DR FILING DATE: 2002-10-09
DR APPLICATION NUMBER: 60/381,038
DR FILING DATE: 2002-05-16
DR APPLICATION NUMBER: 60/328,056
DR APPLICATION NUMBER: 60/328,056
DR APPLICATION NUMBER: 60/328,056
DR FILING DATE: 2001-10-09
       APPLICATION NUMBER: 60/373,260
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Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
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Malyankar, Uriel M.
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Anderson, David W.
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; TYPE: PRT
; ORGANISM: Homo 8
US-10-262-511-86
                SEQ ID NO 6
LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (95)...(96)
OTHER INFORMATION: Xaa c:
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CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/861,205
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/684,254
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/343,809
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1998-12-04
PRIOR FILING DATE: 1997-12-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 86
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Crooke, Stanle APPLICANT: Lima, Walter APPLICANT: Wu, Hongjiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ISPH0725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H and Compositions And Uses Thereof
NAME/KEY: misc_feature
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                                               can
                                            be any naturally occurring amino acid
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Pred. No. 2.8e-149;
2; Mismatches 3;
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240

180

120

60

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PRIOR APPLICATION NUMBER: US 60/67,458
PRIOR PILING DATE: 1997-12-04
PRIOR PILING DATE: 1997-12-04
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 09/684,254
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
ILENORUMENT
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; OTHER INFORMATION: Xaa can be FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (155)..(155)
; OTHER INFORMATION: Xaa can be US-10-358-439-6
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 268; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Crooke, Stanley T
APPLICANT: Lima, Walter
APPLICANT: Lima, Walter
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Methods of Using Mammalian RNase H
FILE REFERENCE: ISPH-0520
CURRENT APPLICATION NUMBER: US/09/781,712B
CURRENT FILING DATE: 2001-02-12
                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      LENGTH: 286
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                     FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
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Pred. No. 1.1e-138;
0; Mismatches 18;
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Pred. No. 7.2e-149;
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RESULT 8 US-09-781-712B-8

Sequence 8, Application US/09781712B Publication No. US20040180433A1 GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T APPLICANT: Lima, Walter

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PRIOR APPLICATION NUMBER: US 60/067,458
PRIOR FILING DATE: 1997-12-04
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 09/684,254
PRIOR APPLICATION NUMBER: US 09/684,254
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PACENTIN VETSION 3.1
SEQ ID NO 7
IENOTH: 206
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Best Local (
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APPLICANT: Lima, Walter
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Methods of Using Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ISPH-0520
CURRENT APPLICATION NUMBER: US/09/781,712B
CURRENT FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                            TNQRAEIHAACLAIEQALTQNINLLVLYTDSMFTINGITNWVQGWLLNGWLTSAGLEVIN
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APPLICANT: Lima, Walter
APPLICANT: Lima, Walter
APPLICANT: Wu, Hongjlang
TITLE OF INVENTION Wethods of Using Mammalian RNase H and Compositions Thereof
FILE REFERENCE: ISPH-0520
CURRENT APPLICATION NUMBER: US/09/781,712B
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: US 60/067,458
PRIOR FILING DATE: 1997-12-04
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 09/684,254
PRIOR FILING DATE: 2000-10-06
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
I-FNCTH: 286
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US-09-781-712B-9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-712B-8
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CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: US 60/067,458
PRIOR FILING DATE: 1997-12-04
PRIOR PPLICATION NUMBER: US 09/203,716
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR PRILING DATE: 1999-06-30
PRIOR PILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 09/684,254
PRIOR APPLICATION NUMBER: US 09/684,254
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09781712B Publication No. US20040180433A1 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
-09-781-712B-9
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TITLE OF INVENTION: Methods of Using Mammalian RNase H
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Pred. No. 6.3e-137;
2; Mismatches 20;
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CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: US 60/067,458
PRIOR FILING DATE: 1997-12-04
PRIOR APPLICATION NUMBER: US 09/203,716
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR APPLICATION NUMBER: US 09/343,809
PRIOR APPLICATION NUMBER: US 09/684,254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09781712B Publication No. US20040180433A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 11
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 263; Conservative
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Best Local
                                                                                                                                                                                                                                                                                                           Matches 208;
                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Lima, Walter
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Methods of Using Mammalian RNase H and Compositions Thereof
FILE REFERENCE: ISPH-0520
FILE REFERENCE: MIMMERR: US/09/781,712B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mus
                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                   121 SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
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                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK 60
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                        TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                        FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
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  TNORAEIHAACLAIMOALAONISLLVLYTDSMFTINGITNWVQGWLLNGWRTSTGLDVIN
                                                                                                                                                       FATEDEAWAFVRSSSSPDGSLGQESAHEQLSQALTSLRPREPL-GEGEELPEPGPLHTRQ
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                         70.3%; Score 1086.5; DB 12 72.7%; Pred. No. 4.8e-104; tive 22; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 285;
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; ORGANISM: Homo sapiens
US-10-262-511-78
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PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
                                Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 78
LENGTH: 203
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CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 3001-10-02
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FILLING DATE: 2002-04-17
RAPPLICATION NUMBER: 60/373,826
FILING DATE: 2002-04-19
RAPPLICATION NUMBER: 60/327,435
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/328,056
                                                                                                                                                                                                                                                                                                              FILING DATE: 2002-10-09
APPLICATION NUMBER: 60/381,038
FILING DATE: 2002-05-16
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Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
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Millet, Isabelle
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Anderson, David W.
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Kekuda, Ramesh
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dinger, Shlomit R.
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APPLICANT: Leach, Martin D.

APPLICANT: Agee, Michele L.

APPLICANT: Agee, Michele L.

APPLICANT: Berghs, Constance

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-462C

CURRENT APPLICATION NUMBER: US/10/262,511

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: 60/326,483

PRIOR APPLICATION NUMBER: 60/326,483

PRIOR APPLICATION NUMBER: 60/373,815

PRIOR APPLICATION NUMBER: 60/373,815

PRIOR PILING DATE: 2001-00-09

PRIOR APPLICATION NUMBER: 60/377,917

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/381,642
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Best Local S
Matches 201
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APPLICANT:
APPLICANT:
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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FILING DATE: 2002-05-17
APPLICATION NUMBER: 60/328,029
FILING DATE: 2002-10-09
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Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
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Pena, Carol E.
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Rastelli, Luca
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Anderson, David W
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Spytek, Kimberly A.
Edinger, Shlomit R.
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; ORGANISM: Homo sapiens
US-10-262-511-80
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-262-511-82
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Smithson,
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Best Local Similarity 70.3%;
Matches 201; Conservative
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SEQ ID NO 80
                                                                                 APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
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                                                 APPLICANT:
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                                   PPLICANT
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R FILING DATE: 2002-05-16

DR APPLICATION NUMBER: 60/328,056

DR FILING DATE: 2001-10-09

DR APPLICATION NUMBER: 60/373,260

DR FILING DATE: 2002-04-17

DR APPLICATION NUMBER: 60/373,826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
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                                                                                                                                                                                                                                                                                                                         Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
                                                                                                                                                                                                               Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Stone, David J
Pena, Carol E.
                                                                                                                 Zerhusen, Bryan D.
Anderson, David W.
                                                                                                                                                   Gorman, Linda
                                                                                                                                                                                   Ellerman, Karen
Malyankar, Uriel M.
                              Miller, Charles E.
Rastelli, Luca
                                                                                   Catterton, Elina
                                                                 Weizhen
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                                                                                                                                                                                                                                                                      Xiaojia (Sasha)
                                                                                                                                                                   Tatiana
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                                                                                                                                                                                                                                                                                                                                                                           Glennda
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RESULT 14
US-09-861-205-5
; Sequence 5, Application US/09861205
; Patent No. US20020076712A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Lima, Walter F.
; APPLICANT: Wu, Hongjiang
; TITLE OF INVENTION: Human RNase H Co
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; ORGANISM: Homo sapiens
US-10-262-511-82
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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 82
LENGTH: 195
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Best Local Similarity
Matches 188; Conserv
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/262,511 CURRENT FILING DATE: 2003-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: 60/328,029
OR FILING DATE: 2002-10-09
OR APPLICATION NUMBER: 60/381,038
OR FILING DATE: 2002-05-16
OR APPLICATION NUMBER: 60/328,056
OR FILING DATE: 2001-10-09
OR FILING DATE: 2001-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                              40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 AALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFVRK 73
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                                                                                                                                                                                                                                                                                                                                                                IEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQG 253
                                                                                                                                                                                                                                                  MDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
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Leach, Martin D.
Agee, Michele L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 3.7e-93;
2; Mismatches 0
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FILE REFERENCE: ISPH-0333

Compositions

and Uses Thereof

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Sequence 5, Application US/10054313
Publication No. US20020110892A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Crooke, Scanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-0333
CURRENT APPLICATION NUMBER: US/10/054,313
CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: 09/203,716
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
LENGTH: 216
TYPE: PRT
CRGANISM: Mus musculus
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US-10-054-313-5
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-861-205-5
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CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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141 VYYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
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                                                                                             EGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKPSVEPAPPVSRDTFSYMGDFV 140
                                                                                                                                                                GSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFVRKSASPEVS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NISKLVLYTDSMFTINGITNWVQGWKKNGWRTSTGKDVINKEDFMELDELTQGMDIQWMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQWMH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQ 200
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                                                                                                                                        GICGLGMFYAVRRGRRPGVFLSWSECKAQVDRFPAARFKKFATEDEAWAFVRSSSSPDGS 60
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                                                             KGQESAHEQKSQAKTSKRPREPL-----
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                                                                                                                                                                                                                 Score 959; DB 13;
Pred. No. 5.7e-91;
20; Mismatches 19;
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RESULT 17
US-10-358-439-2
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US-10-358-439-5
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CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/861,205
PRIOR PILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/684,254
PRIOR APPLICATION NUMBER: 09/634,809
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 13
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LENGTH: 216
TYPE: PRT
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Best Local Similarity
Matches 177; Conserv
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APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H and Compositions And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2
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IPGHSGFVGNEE 216
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Sequence 2, Application US/10358439
Publication No. US20030144496A1
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Tima Walter F.

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CURRENT APPLICATION NUMBER: US/09/861,205
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEO ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 293
TYPE: PAT
ORGANISM: Gallus sp.
US-09-861-205-2
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CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: 09/861,205
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/343,809
PRIOR PILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/303,716
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
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SEQ ID NO 2
LENGTH: 293
Query Match
Best Local Similarity
Matches 172; Conserv
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APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-0333
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TITLE OF INVENTION: Human RNase H and Compositions And Uses Thereof
FILE REFERENCE: ISPH0725
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ORGANISM: Gallus sp.
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56.9%; ilarity 57.3%; Conservative 3:
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57.7%;
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  32;
Score 880; DB 9; Length 293; Pred. No. 1.4e-82; Mismatches 72; Indels
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Pred. No. 8.8e-83;
4; Mismatches 69;
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Gallus :
US-10-054-313-2
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Publication No. US20020110892A1
GENERAL INFORMATION:
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Best Local
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APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILLE REFERENCE: ISPH-033
CURRENT APPLICATION NUMBER: US/10/054,313
CURRENT FILING DATE: 2001-10:
EVALUATION NUMBER: EARLI-ER
PRIOR APPLICATION NUMBER: EARLI-ER
PRIOR APPLICATION NUMBER: EARLI-ER
PRIOR FILING DATE: EARLI-ER APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: EARLI-ER FILING DATE: 1998-12-02
NUMBER OF SEQ. ID NOS: 12
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APPLICANT: Lima,
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                                                                                                                                      TNEEHTVRRAKH--DEEQSTPVVSEAKFSYMGEFAVVYTDGCCSGNGRNRARAGIGVYWG
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                                                                                                                                                                                                             FATEKEAWAFVGAGPPDGQQSAPAETHGASAVAQENASHREEPETDVLCCNACKRRYEQS 114
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KTNGWRTSSGGSVINKEDFQKLDSLSKGIEIQWMHIPGHAGFQGNEEADRLAREGASKQK
                                                                    PGHPLNISERLPGRQTNQRAEIHAACKAIEQAKSQNIKKLIIYTDSKFTINGITSWVENW
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                                                                                                                                                                                                                                                                                                                                                                                       Length 293;
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RESULT 20 US-10-262-511-84 ; Sequence 84, Application US/10262511 ; Publication No. US20040038223A1

APPLICANT:

Millet, Isabelle Peyman, John A. Kekuda, Ramesh INFORMATION:

Smithson,

Glennda

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                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-262-511-84
                                                                                                                     Query Match
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 84
                                                                                                                   Matches
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CURRENT FILING DATE: 2003-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 21402-462C
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                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/326,483
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                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR FILING DATE: 2001-10-02
OR APPLICATION NUMBER: 60/373,815
OR FILING DATE: 2002-04-19
OR APPLICATION NUMBER: 60/327,917
OR FILING DATE: 2001-10-09
OR APPLICATION NUMBER: 60/381,642
OR APPLICATION NUMBER: 60/381,642
OR FILING DATE: 2002-05-17
                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2002-04-17
APPLICATION NUMBER: 60/373,826
FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/381,038 FILING DATE: 2002-05-16 APPLICATION NUMBER: 60/328,056
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-10-09
APPLICATION NUMBER: 60/373,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/327,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/328,029
                      197
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Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
AKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDI
                                                                     GDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQ 196
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                                                 GDFVVVYTDGCCSSNGRRRPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQ
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gorman, Linda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ellerman, Karen
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                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                   Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weizhen
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                                                                                                                               51.2%;
                                                                                                                Score 792; DB 12;
Pred. No. 7.9e-74;
1; Mismatches 0;
                                                                                                                  0,
                                                                                                                                                Length 152;
                                                                                                                   Indels
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                                                                                                                Gaps
                  256
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR TILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5383
LENGTH: 369
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US-10-369-493-5383
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US-09-992-738-1
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US-10-369-493-5383
                                                       Sequence 1, Application US/09992738
Patent No. US20020160486A1
GENERAL INFORMATION:
APPLICANT: Wu, Hongjiang
APPLICANT: Lima, Walter F.
APPLICANT: Crooke, Stanley T.
APPLICANT: Crooke, Stanley T.
FILE REFERENCE: ISPH-0614
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5383, Application US/10369493 Publication No. US20030233675A1
CURRENT APPLICATION NUMBER: US/09/992,738
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/248,950
                                                                                                                                                                                                                                                                                                              304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 HDTYYAVARGHSVGVFTNYNEVKEHIKNYPQPLHKKWSTLEEAIAYFHKYYEGKEEAKKA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 FYGVAHGFKRGVFTEWAEAKKQIDKFPQPVYKKFETEEEAQKYVDDRKPKKVESTFPEST
                                                                                                                                                                                                                                                                                                              HGWKRKGWKTSTGSEVLNQDVLMKIDNLRQKLKVKFLHVRGHAGIDGNEKADELARKGAQ
                                                                                                                                                                                                                                                                                                                                                    QGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                    YWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEPAPPVSRDTFS------YMGDFVVVYTDGCCSSNGRRKPRAGIGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSTSSATRKRTHEGTKFTEAKKMKTEEEVIDPEFANAPVVYTDGACSSNGTKNAKAGWGV
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;; Pred. No. 8.9e-37;
44; Mismatches 103;
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US-10-369-493-13271
; Sequence 13271, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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SEQ ID NO 13271
LENGTH: 300
TYPE: PRT
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                           ORGANISM: Aspergillus nidulans -10-369-493-13271
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TYPE: PRT
ORGANISM: Homo sapiens
-09-992-738-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                     Local Similarity
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                      114 YAKHMKPSVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151;
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                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 -----DAWA-VRKSAS---VSGH--NHG---SAKASKR----RDGDGHSA---YAKHMK- 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinkle, Gregory J.Slater, Steven C.Goldman, Barry S.Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYMGPGHPLNVGIRLPGRQ 180
                                                                                                                                                              FYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAF--VRKSAS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
 LPKH---SQKDHPACS---
                                                                    TSRGSGLDERYPERSAGQSVRTGRGPFTPRCGGWVRSECDP--RSKDPARLSTRHQSRKQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RGRNRAHAACKAAKNNKVY------DSM---NG--NWV--GKKNGWK-SAGK--VN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNORAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SVAVSRD--SYMGD-VVVY-DGCCSSNGRRR-RAG-GVYWG-GH--NVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSW----AHRVAAA---CRRGSRG-GM-YAVRRGRK-GV---WN-CRA-VDR--AARKKA
                                                                                                                                             FYAIQRGHKPGVYTNWANAQEQIRGFQKPRYKKFSTREEAEEFCEARRGARSVCDFYRHQ 60
                                                                                                                                                                                                                  21.7%; Score 335; DB 15; ilarity 30.7%; Pred. No. 6.1e-26; Conservative 37; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VARGMD--WMHV-GHSG--GN--ADR--ARGAK 187
                                                                                                       PEVSEGHENOHGQ------ESEAKPGKRLREPLD-GDGHESAQP 113
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Pred. No. 1.6
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VFTTDGSSLRNGRVQAMAGVGVYFGPGDSRFVS 164
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                                                                                                                                                                                                                                                       Length 300;
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                                                                                                                                                                                                                    86;
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
FILL OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3170
LENGTH: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(275)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3170
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Best Local Similarity
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            223
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GEEVSNODLIVAIRKKIDTRDRKAAETKFVWVKGHGTDEGNIAADMLAVKGA
                                                GKEVINKEDFVALE-----RLTQGMDIQWMHVPGHSGFIGNEEADRLAREGA 281
                                                                                                                                PGR-QTNQRAEIHAACKAIEQ-AKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSA 234
                                                                                                                                                                                                                                                     SGRDRXPASHCSGRASKSSRKARKTGATQSAHQAQEALDDASKP---
                                                                                                                                                                                                                                                                                         EGHENOHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKPSVEPAPPVSRDTFSYMGDFV 140
                                                                                                                                                                                                                                                                                                                                   FYGVAVGRTPGVYTDWSIAQQEVVGWKNPKYKKFETRAEAEEFVRQWSGKPSSPSRQGTT
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                                                                                            QGPVQTNQRAELTAVLRALEAIPDTQNCE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMD--
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                                                                                        -LRTDSOYTINCVTSWYKKWMKNEWRNTK
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                                                                                                                                                                                                               ----PLNVGIRL 176
                                                                                                                                                                                                                                                                                                                                                                                                                     56; Gaps
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; Sequence 2540, Application US/10369493 ; Publication No. US20030333675A1 ; GENERAL INFORMATION: ; APPLICANT: Cao, Yongwei

RESULT 25 US-10-369-493-2540

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NO.540
LENGTH: 325
TYPE: PRT
CRANISM: Schizosaccharomyces pombe
PEATURE:
NAME/KEY: unsure
J. LOCATION: (1): (325)
OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2540
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Search completed: October 7, 2004, 08:19:49
Job time : 132 secs
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                                                                                           282 NLDLINRASDLMSDRNVSLEYVKGHSTDYGNQQADMLARRGASE 325
                                                                                                                   240 NKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
                                                                                                                                                                                  226 QTNNRAELQAIILALENTS----GDLTIRSDSNYSIKSLTTWLPKWKKNDFKTSNSQPVK 281
                                                                                                                                                                                                                    180 QTNQRAEJHAACKAJEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVI 239
                                                                                                                                                                                                                                                                           179 -----IACSDRQVVYADGSSLRNGKKGAVAGCGVFFGNDDPRNISVPLAGEE 225
                                                                                                                                                                                                                                                                                                      121 SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYMGPGHPLNVGIRLPG-R 179
                                                                                                                                                                                                                                                                                                                                                                       128 RSTTSYGYSPYSSSSSNYSARHSDKYRKKISRSYSTEKDIEIFSNDTHEKS----- 178
                                                                                                                                                                                                                                                                                                                                                                                                                     73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KSASPEVSEGHENQHGQE-SEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
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Minimum
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Perfect score:
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Crooke, Stanley T.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and
FILE REFERENCE: ISPH-033
CURRENT APPLICATION NUMBER: US/09/684,254
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 286
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APPLICANT: Lima, Walter F.
APPLICANT: Lima, Walter F.
APPLICANT: Lima, Walter F.
APPLICANT: Win, Hongiang
TITLE OF INVENTION: Human RNase H Compositions and
FILE REFERENCE: ISPH-033
CURRENT APPLICATION NUMBER: U$/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
; TYPE: PRT; ORGANISM: Homo sapiens US-09-684-254-1
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US-09-684-254-1
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; TYPE: PRT
; ORGANISM: Homo sapiens
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Patent No. 6001653
GENERAL INFORMATION:
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Local Similarity 100.0%; Pred. No. 4.2e-168;
hes 286; Conservative 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Artificial Sequence
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Patent No. 6617442
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human Rnase H1 and Oligonucleotide Compositions Thereof
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CURRENT APPLICATION NUMBER: US/09/409,926
CURRENT FILING DATE: 199-09-30
NUMBER OF SEQ ID NOS: 33
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                                                                                               TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                         SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
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                   KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 286
                                                                        TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
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100.0%; Pred. No. 4.2e-168;
tive 0; Mismatches 0;
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APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Use
FILE REFERENCE: ISPH-0333
CURRENT APPLICATION NUMBER: US/09/684,254
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 216
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US-09-684-254-5
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APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-033
CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52
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Patent No. 6001653
GENERAL INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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               Query Match
Best Local Similarity
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TYPE: PRT
ORGANISM: Mus musculus
-09-203-716-5
Matches 177;
                                                                      TYPE: PRT
ORGANISM: Mus musculus
-09-684-254-5
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o. 6376661
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Conservative
                 62.0%; Score 959; DB 4; 70.2%; Pred. No. 3.3e-101;
20;
 Mismatches
                                   Length 216;
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APPLICANT: Lima, Walter F.
APPLICANT: Lima, Walter F.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OP INVENTION: Human Rnase H1 and Oligonucleotide Compositions Thereof
FILE REFERENCE: ISIS4186
CURRENT APPLICATION NUMBER: US/09/409,926
CURRENT APPLICATION NUMBER: US/09/409,926
CURRENT FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 216
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-409-926-4
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Best Local Similarity
205
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                                                            NISKLVLYTDSMFTINGITNWVQGWKKNGWRTSTGKDVINKEDFMELDELTQGMDIQWMH
                                                                                 NINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQWMH
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                                                                                                                                                                                                                                                                                                              62.0%; Score 959; DB 4; 70.2%; Pred. No. 3.3e-101; tive 20; Mismatches 19;
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US-09-409-926-2
; Sequence 2, Application US/09409926
; Patent No. 6617442
; GENERAL INFORMATION:

RESULT 7

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US-09-203-716-2
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APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human
                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09203716 Patent No. 6001653
                                                                                                                       Matches 172;
                                                                                                                                                         Query Match
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APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-0333
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: -09-409-926-2
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SOFTWARE: PatentIn Ver.
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CURRENT APPLICATION NUMBER: US/09/409,926
CURRENT FILING DATE: 199-09-30
NUMBER OF SEQ ID NOS: 33
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 PGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 TNEEHTVRRAKH--DEEQSTPVVSEAKFSYMGEFAVVYTDGCCSGNGRNRARAGIGVYWG
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                                               N
           FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTNGWRTSSGGSVINKEDFQKLDSLSKGIEIQWMHIPGHAGFQGNEEADRLAREGASKQK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AKHMKPSVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FATEKEAWAFVGAGPPDGQQSAPAETHGASAVAQENASHREEPETDVLCCNACKRPYEQS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGD---GHESAQPY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRWL-----VALLSHSC-FVSKGGGMFYAVRKGRQTGVYRTWAECQQQVNRFPSASFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGHPLNISERLPGRQTNQRAEIHAACKAIEQAKSQNIKKLIIYTDSKFTINGITSWVENW
                                                                                                                       Conservative
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                                           VALLSHSC-FVSKGGGMFYAVRKGRQTGVYRTWAECQQQVNRFPSASFKK
                                                                                                                                    56.9%;
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                                                                                                      Score 880; DB 3; Leng... Pred. No. 5.5e-92; Indels
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Pred. No. 3.2e-92;
                                                                                                                                                      Length 293;
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           106
     GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236
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                                US-09-540-236-3622
                                                      RESULT 10
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Sequence 3622, Ap
Patent No. 667391
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CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/203,716
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09684254
Patent No. 6376661
GENERAL INFORMATION:
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Best Local
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APPLICANT: Lima, Walter F.
APPLICANT: Mu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ISPH-0333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 293
TYPE: PRT
ORGANISM: Gallus sp.
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                                                                                                                                         226
                                                                                                                                                                                                                                               115 TNEEHTVRRAKH--DEEQSTPVVSEAKFSYMGEFAVVYTDGCCSGNGRNRARAGIGVYWG
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                                                                                                                              KKNGWKTSAGKEVINKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSE 285
                                                                                                                                                                                          PGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGW
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                                                                                                       KTNGWRTSSGGSVINKEDFOKLDSLSKGIEIQWMHIPGHAGFOGNEEADRLAREGASKOK
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                                                                                                                                                                                                                                                                                                                  FATEKEAWAFVGAGPPDGQQSAPAETHGASAVAQENASHREEPETDVLCCNACKRRYEQS 114
                                                                                                                                                                                                                                                                                                                                                 FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGD-------
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                  Application US/09540236
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Pred. No. 5.5e-92;
2; Mismatches 72
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; ORGANISM: M.catarrhalis
US-09-540-236-3622
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US-09-203-716-3
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APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISBH-0333
FILE REFERENCE: ISBH-0333
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NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3622
LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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LENGTH: 348
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Best Local Similarity 39.5%; Pred. No. 3e-22;
Matches 62; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 FVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 MGDFVVVYTDGCCSSNGRRKPRA-GIGVY------WGPGHPLNVGIRLPGRQTNQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                          RAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKED 243
                                                                                                                                                                                                                            IESKIFNNWKDCQAYVKHKRGITFKKFEDQLAAENFISGMSAHDYKLMNISKESFESKYK 177
                                                                                                                                                                                                                                                                                                                                               ASPEVSEGHENOHGOESEAKPGKRLREPLDGDGHESA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WORLDOLTONRIIDWOWIKGHAGHAGNEMADQLANKG 154
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                                                              IEAVSEALKKIWEKLTNEKEKVNYQIKTDSEYVTKLLNDRYMTYDNKKLEGLPNSDLIVP
                                                                                                                                                                                    VSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVG-IRLPGRQTNQRAE 186
                                                                                                                                                                                                                                                                                                                                                                                       GNFYAVRKGRETGIYNTWNECKNQVDGYGGAIYKKFNSYEQAKSFLGQPNTTSNYGSSTH 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMELMAAITALEATPAQ--IPLQLWTDSGYVKDGITQWIGGWKLRGWKKADGKPVLNQDL 117
                                                                                                    IHAACKAIEQ--AKTQNINKLVLY---TDSMFTINGITNWVQGWKKNGWKTSAGKEVI--
                                                                                                                                            LSSNTM--YNKSMNVYCDGSSFGNGTSSSRAGYGAYFEGAPEENISEPLLSGAOTNNRAE
                                                                                                                                                                                                                                                                                                       AGGQVSKPHTTQ-----KRVHRRNRPLHYSSLTSSSACSSLSSANTNTFYSVKSNVPN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                  ----QPYAKH------ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.1%; Score 249.5; DB 3; 26.0%; Pred. No. 7.8e-20;
NKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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Patent No. 6376661
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                                                                                                                                                                                                                                                               Sequence 3, Application US/09409926 Patent No. 6617442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                  SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                              GENERAL
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                                                                                                  FILE REFERENCE: ISIS4186
CURRENT APPLICATION NUMBER: US/09/409,926
CURRENT FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 33
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CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/203,716
                                                                                                                                                                        APPLICANT: Wu, Hongjiang TITLE OF INVENTION: Human
                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions
FILE REFERENCE: ISPH-0333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-12-02
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     LENGTH: 348
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Saccharomyces
FEATURE:
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                                                                                                                                                                                                                                                INFORMATION:
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                                                                                     PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                        LVQRFVKVKKYYELNKECF----KNNGKFQIEW--VKGHDGDPGNEMADFLAKKGASR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVG-IRLPGRQTNQRAS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGQVSKPHTTQ-----KRVHRRNRPLHYSSLTSSSACSSLSSANTNTFYSVKSNVPN 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IHAACKAIEQ--AKTQNINKLVLY---TDSMFTINGITNWVQGWKKNGWKTSAGKEVI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSNTM--YNKSMNVYCDGSSFGNGTSSSRAGYGAYFEGAPEENISEPLLSGAQTNNRAE
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                                                                                                                                                                                                           Crooke, Stan
Lima, Walter
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                                                                                                                                                                                                           Stanley T. 
alter F.
                                                                                                                                                                      Human Rnase H1 and Oligonucleotide Compositions Thereof
                                                                                                                                                                                                                                                                                                                                                                                                    -NKEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQ 283
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Pred. No. 7.8e-20;
38; Mismatches 112;
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Description of Artificial Sequence: No. 6617442el

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US-09-252-991A-30209
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30209
                                                                                                                                                                                                                                                                                                         Matches
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Patent No. 6551795
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 424
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 SAGAHAGGESQPARFRNLGMTDKEQVVIYTDGACKGNPGRGGWGALLLYKGAERELWG-G
                                                                                                                    SA----
                                                                                                                                                                                                                                HRADSAR -- CAPGAAAAGRGHRLRRGR ----LAAQRTCRG---RGPAATRPGFLPVASPS
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                                                                            TALRVLSSAACVGSLAIAPGSPGALGRRLAVFGRRLLSIGGTQAGRGVAPVAPEQARTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MARC J. Rubenfield et al.
MARC J. Rubenfield et al.
VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: APPRICINGSA FOR DIAGNOSTICS AND THERAPEUTICS
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MBER: US 60/074,788
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                                   FSYMG----DFVVVYTDGCCSSNGRRKPRAGIGVY------WGPG 167
                                                                                                                    ----QPYAKHMK----
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                                                                                                                                                                                                                                                                                                       Score 241; DB 4;
Pred. No. 9.9e-19;
6; Mismatches 126
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Pred. No. 7.8
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                                                                                                                  -----PSVEPAPPVSRDT--
                                                                                                                                                                                                                                                                                                                                          Length 424;
                                                                                                                                                                                                                                                                                                       Indels 102;
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                                                                                                                                                                                                                                               RESULT 16
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US-09-199-637A-157
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NUMBER OF SEQ ID NOS:
SEQ ID NO 5891
LENGTH: 502
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Best Local
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                          Patent No. 6562958
                                                                                                                                                                                                          Sequence 5891,
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SEQ ID NO 157
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APPLICANT:
                                                     APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
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APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 AGIGVY-----WGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQNINKLVLYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 PLDGDGHESAQPYAKHMKPSVEPAPPVSRDTFSYMG----DFVVVYTDGCCSSNGRRKPR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 HPLNVGIRLPGRQTNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157, Application US/09199637A
o. 6355411
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                                                                                                                                                                                                                                                                                                         ERADQLANRGVAE 263
                                                                                                                                                                                                                                                                                                                                        EEADRLAREGAKQ 283
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Goodman, Howard M.
Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                            Application US/09328352
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31.6%; Pred
3--- 29;
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Pred. No. 2.1e-18;
9; Mismatches 74
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ACINETOBACTER

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; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-5891
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US-09-684-254-4
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Best Local Similarity
Matches 52; Conserv
GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions
FILE REFERENCE: ISPH-0333
CURRENT APPLICATION NUMBER: US/09/684,254
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/203,716
                                                                                                                                                                                   Sequence 4, Application US/09684254 Patent No. 6376661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions
FILE REFERENCE: ISPH-0333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 13.5%; Score 208.5; DB 3; Length Local Similarity 36.6%; Pred. No. 1.1e-15; see 52; Conservative 16; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKT 199
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                                                                                                                                                                                                                                                                                                                                               HVPGHSGFIGNEEADRLAREGA 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEIFTDGSCLGNPGPGGYGAILRYRGREKTFSAGYT---RTTNNRMELMAAIVALEALKE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTNNRMELTAAIEGISFCPPD--AQLIVWTDSNYVKQGITEWIHGWKKKNW-----KDVK 137
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31.5%; Pred. No. 7e-16;
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                                                                                                                           US-09-489-039A-12690
  GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                 Sequence 12690, Application US/09489039A Patent No. 6610836
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US-09-684-254-4
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wi, Hongjiang
TITLE OF INVENTION: Human Rnase H1 and Olig
FILE REFERENCE: ISIS4186
CURRENT APPLICATION NUMBER: US/09/409,926
CURRENT FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 33
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Best Local S
Matches 52
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SEQ ID NO 5
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NUMBER OF SEQ ID NOS: 12
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TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 155
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: No. 6617442el Sequence
                                                                                                                                                                                                                                                                                                                                 y Match 13.5%; Score 208.5; DB 4; Local Similarity 36.6%; Pred. No. 1.1e-15; hes 52; Conservative 16; Mismatches 69;
                                                                    120
                                                                                                                                                                                     200 QNINKLVLYIDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQMM 259
                                                                                                                                                                                                                                                                                      140 VVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKAIEQAKT
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o. 6617442
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                                                                    WVKGHAGHPENERCDELARAAA 141
                                                                                                           HVPGHSGFIGNEEADRLAREGA 281
                                                                                                                                                     H--CEVILSTDSQYVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWE 119
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36.6%; Pred. No. 1.1e-15;
1tive 16; Mismatches 69
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RESULT 22
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APPLICANT: CARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6179
SEQ ID NO 6179
                      Sequence 8, Application
Patent No. 5891637
GENERAL INFORMATION:
APPLICANT: Ruppert,
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
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TYPE: PRT
      APPLICANT: Ruppert, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                  182 NQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINK 241
                                                                                                                                                                                                                                                                                                                 134 SYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ------T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 VVVYTDGCCSSNGRRKPRAGIGVYWGPG-------HPLNVGIRLPGRQTNQRAEI 187
                                                                                                                                                                                                                 47 NNRMELLAAIVALEALKFP--CKITLTTDSQYVRQGITKWIHSWKKRQWRKADKSPVLNV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 MAAIVALEALKEH--CEVVLSTDSQYVRQGITQWIHNWKKRGWKTAEKKPVKNVDLWQRL 152
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                                                                                                                                                  DLWKRLDKAIERHEIEWHWVKGHAGHDENERCDELAKAAAQ 145
                                                                                                                                                                                                                                                                                AFMHKQVEIFTDGSCLGNP------GPG---GYGAILRYQQHEKTLSEGFFMTT
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Siegfried J.W. Construction of Full-Length cDNA Libraries
                                                                     US/08929967
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Pred. No. 4.8e-14;
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; OTHER INFORMATION: gag-pol protein US-09-309-572-13
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                                                                                                   EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 1737
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 13,
                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09309572 Patent No. 6440730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
                                              LENGTH: 1737
TYPE: PRT
ORGANISM: Moloney murine leukemia virus
                                                                                                                                                                                                                                                                          FILE REFERENCE: P50489
                                                                                                                                                                                                                                                                                           APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral hybrid vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                       FEATURE:
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LENGTH: 1079 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLSI--IHCPGHQKGHSAEARGNRMADQAARKAA 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTDGSSLLQEGQRKAGAAVTTETEVIWAKA-----LPAGTSAQRAELIALTQALKWA 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QHGQESEAKPGKKLREPLDGDGHESAQPYAK--HMKPSVEPAP-PVSRDTFSYMGDFVVV 142
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28.5%; Pred. No. 1e-07;
ative 33; Mismatches
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GENERAL INFORMATION:

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RESULT 24
US-09-718-096-13
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US-08-929-967-7

US-08-929-967-7

; Sequence 7, Application US/08929967

; Patent No. 5891637
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SEQ ID NO 13
LENGTH: 1737
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GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-11-26
PRIOR APPLICATION NUMBER: EP 99250415.9
PRIOR FILING DATE: 1999-11-25
PRIOR APPLICATION NUMBER: US 09/309,572
PRIOR FILING DATE: 1999-05-11
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CURRENT APPLICATION NUMBER: US/09/718,096
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: DE 19856463.5
PRIOR FILING DATE: 1998-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Moloney murine leukemia virus FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
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Best Local :
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time : 35 secs
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/929,967
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 665 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1
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MEDIUM TYPE: 3.5 inc
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TITLE OF INVENTION: Construction of Full-Length cDNA Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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(c) 1993 - 2004 Compugen Ltd.
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AAR799151

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Aar13113

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Aar14206

Aar14207

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Add11344

Add1134

Aar20663

Aau48190

Abm44709

Abm44709

Abm44709

Abm4901947

Aaw39272

Aaw39272

Aaw3017947

Aab1094

Aay117947

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Aab88527
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528 N. gonori
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151 Fibonucle
263 Ribonucle
264 Photorhab
265 Propojonib
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267 Porcine r
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262 FIV-Rob
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264 ElV-2 Rob
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66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel human RNase H polypeptide and nucleic acid which can be used to cleave the RNA strand of oligonucleotide-RNA duplexes and to develop agents for enhancing the efficiency of antisense therapy. The products of the invention are useful in defining the interaction of human Type 2 RNase H and antisense oligonucleotides and identifying methods for enhancing this interaction so that antisense oligonucleotides are more effective at inhibiting their target mRNA. The products can be used for enhancing the efficacy of antisense oligonucleotide therapies. This sequence represents the human type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human RNase H polypeptide and nucleic acid, used to develop agents for enhancing the efficiency of antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type 2 RNase H; oligonucleotide-RNA duplex; cleavage; antisense therapy; interaction; target mRNA; human.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 28-29; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1997;
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                                                                                                             121 SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
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                     TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                            SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                                     FATEDEAWAFVRKSASPEVSEGHENOHGOESEAKPGKRLREPLDGDGHESAOPYAKHMKP
                                                                                                                                                               FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                                                                                                                                                                                  MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK
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Pred. No. 1.5
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Abg19846 Novel hum
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric oligonucleotides that can serve as substrates for human RNase H1, useful for enhancing the effectiveness of antisense gene therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-343164/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; RNase H gene therapy.
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                                                                                                                          TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                                           SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                                                                                                                    FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                                                                                                                                                                                                                                   FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
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                                                      KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 286
                                                                                                                                                                                   SVEPAPPVSRDTFSYMGDFVVVYYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
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               KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
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286

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for promoting the inhibition of the expression of a protein comprising employing a mammalian RNase H polypeptide so that cleavage of an RNA strand of an oligonucleotide-RNA complex duplex occurs. Also described is a compound 8 to 50 nucleobases in length targeted to the nucleic acid encoding the human RNase HII polypeptide, where the compound specifically hybridises with and inhibits the expression of a human RNase HII polypeptide is useful for inhibiting the expression of a human RNase HII polypeptide in cells or tissues, as well as for treating an animal with a disease or condition associated with a human RNase HII polypeptide. The method is useful for inhibiting the expression of a protein, particularly for reducing cellular RNA via antisense technology. The present sequence represents human type 2 RNase H given in the exemption of the present sequence represents human type 2 RNase H given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a mammalian, particularly human, RNase H, for treating an animal with a disease or condition associated with a human RNase H, for inhibiting the expression of a protein, or for reducing cellular RNA via
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               technology. The present sequence represent invention the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286
                               TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKXNGWKTSAGKEVIN 240
                                                                                                                                                  SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                                                                                                                                  FATEDBAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
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TNORAEIHAACKAIEOAKTONINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
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ilarity 100.0%;
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Pred. No. 1.5e-148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a mammalian, particularly human, RNase H, for treating an with a disease or condition associated with a human RNase H, for inhibiting the expression of a protein, or for reducing cellular
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                                                                                                                                                                                     Sequence
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              FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                 MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK
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                                                              MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK
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                                                                                                                          Conservative
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                                                                                                                         Score 1526; DB 5;
Pred. No. 1.7e-146;
2; Mismatches 2;
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                                                                                                                                                                Hillman JL,
                                                                       preventing
                                                                          Human RNA-associated proteins useful in diagnosing, treating and preventing cell proliferative, autoimmune, inflammatory and infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-associated protein; RNAAP; human; clone 2073417; cytostatic; immunosuppressive; antiinflammatory; keracolytic; neuroprotective; antiarteriosclerotic; hepatotropic; antipsoriatic; virucide; anti-HIV; antiallergic; antirheumatic; antiarthritic; opthalmological; autoimmune; antimicrobial; cell proliferative disorder; inflammation; cirrhosis; actinic keratosis; bursitis; arteriosclerosis; artherosclerosis; hepatitis; myelofibrosis; primary thrombocythemia; psoriasis; cancer; mixed connective tissue disease; MCTD; HIV; uveitis; Crohn's disease; mixed connective tissue disease; MCTD; HIV; uveitis; Crohn's disease;
The present amino acid sequence is the human RNA-associated protein-16 (RNAAP-16), identified in Incyte clone 2073417, derived from ISLTNOT01
                                     Claim 1; Page 95-96; 123pp; English.
                                                                                                                N-PSDB; AAZ51265
                                                                                                                                                                                                                                21-AUG-1998;
12-JAN-1999;
                                                                                                                                                                                                                                                                      20-AUG-1999;
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                                                                                                                              2000-237651/20.
                                                                                                                                                     LL, Yang J,
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, Baughn MR, Lal
ang J, Lu DAM;
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99US-0115639P
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137. .282
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19. .286
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                                                                                                                                                                                                                                                                                                                                                                                               note= "Potential phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                12-FEB-2001; 2001US-00781712.
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                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                  2002-657606/70
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Use of a mammalian, particularly human, RNase H, for treating with a disease or condition associated with a human RNase H, inhibiting the expression of a protein, or for reducing cellul

reducing cellular

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animal

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RRESULT 7
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02-OCT-2001;
05-OCT-2001;
05-OCT-2001;
                                                                                                                                                                                                                                                                                                                                          human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene thrappy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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Pred. No. 4.2e-146;
2; Mismatches 3;
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19-APR-2002;
19-APR-2002;
22-APR-2002;
16-MAY-2002;
16-MAY-2002;
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17-OCT-2001
18-OCT-2001
22-OCT-2001
24-OCT-2001
24-OCT-2001
29-OCT-2001
01-NOV-2001
17-APR-2002
19-APR-2002
19-APR-2002
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09-OCT-2001;
09-OCT-2001;
09-OCT-2001;
12-OCT-2001;
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17-MAY-2002;
28-MAY-2002;
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2002US-0373824P.
2002US-0373884P.
2002US-0373797P.
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2002US-0381038P.
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2001US-0328029P.
2001US-0328044P.
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Kekuda R, Ju J, ۷A;

2003-381626/36. DB; ADA05725.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics. obesity,

Claim 1; Page 161; 586pp; English

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOVI). Also described: (1) a composition comprising a polypeptide containers, the composition described above; 1) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the above vector; (6) an isolated nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or uncleic acid molecule in a gample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (10) a method of or producing the above polypeptide in a method for producing the above polypeptide. NOVX immunomodulator, cytostatic, nootropic, neuroprotective, antipatkinsonian and antilipamenic activities, and can be used in gene therapy. The collypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease.

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                                                                                                                                                         Use of a mammalian, particularly human, RNase H, for treating with a disease or condition associated with a human RNase H, inhibiting the expression of a protein, or for reducing celluinhibiting the expression of a protein, or for reducing celluinhibiting the expression of a protein, or for reducing celluinhibiting the expression of a protein, or for reducing celluinhibiting the expression of a protein, or for reducing celluinhibiting the expression of a protein of the control of t
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                                                                            8; Page 57-58; 70pp; English.
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Pred. No. 4.2e-146;
2; Mismatches 3;
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present invention describes a method for promoting the inhibition expression of a protein comprising employing a mammalian RNase H

comprising

14-NOV-2001; 2001WO-US043929

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide so that cleavage of an RNA strand of an oligonucleotide-RNA complex duplex occurs. Also described is a compound 8 to 50 nucleobases in length targeted to the nucleic acid encoding the human RNase HII polypeptide, where the compound specifically hybridises with and inhibits the expression of a human RNase HII polypeptide. The compound, which is an antisense oligonucleotide, is useful for inhibiting the expression of a human RNase HII polypeptide in cells or tissues, as well as for treating an animal with a disease or condition associated with a human RNase HII polypeptide. The method is useful for inhibiting the expression of a protein, particularly for reducing cellular RNA via antisense technology. The present sequence represents a human RNase HII protein sequence, given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                             /label= Region III
/note= "Included within this region are the
amino acid residues that form the catalytic
divalent cation binding site, and the basic
                                                                                              binding
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                          /label= Region_I
/note= "Contains the
                                                                                                                                                                                                                                                                                                                                                       enzyme
                                                                                                                                                                                         'label= Region_II
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1. No. 1.1e-145;
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RESULT 10
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            Key
Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human RNase H1 polypeptide comprising mutations compared to wild type human RNase H1 useful for inhibiting expression of selected protein by antisense oligonucleotide targeted to RNA encoding selected protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2000; 2000US-0248950P
                                                                                                                         Mutant RNase
                                                                                                                                                    04-SEP-2002
                                                       Synthetic
                                                                   Homo sapiens.
                                                                                              Human; RNase
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                                                                                                                                                                                                                                                                                                                                                                                                       SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                            KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
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                                                                                                                                                    (first entry)
Location/Qualifiers
1. .73
/label= Region_I
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                                                                                                                                                                                                       protein;
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Pred. No. 3.5e-145;
2; Mismatches 3;
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The present sequence is a mutant RNase H1 sequence. RNase H hydrolyses CC RNA in RNA-DNA hybrids, and the activity of RNase H1 is Mg+2 dependent created by both Mn+2 and the sulphydryl blocking agent N-cethylmaleimide. The amino acid sequence of human RNase H1 displays strong Chomology with RNase H1 from yeast, chicken, E. coli and mouse. This sequence was generated from the wild-type human RNase H1 sequence (ABB83371) by site-directed mutagenesis. It was found that although the conserved amino acid residues of the putative catalytic site and basic substrate-binding domain are required for RNase H activity, deletion of cither the catalytic site or the basic substrate-binding domain did not undetectable rate of cleavage of a heteroduplex substrate, i.e. the mutation ablated the cleavage of a heteroduplex substrate, i.e. the mutation ablated the cleavage activity of the enzyme. Note: The present sequence was not shown in the specification, but was derived from the construction and the sequence shown on Fig 1
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KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
                                                                         TNQRABIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKKGGWKTSAGKEVIN
                                                                                                                                                    SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYMGPGHPLNVGIRLPGRQ
                                                                                                                                                                                                    FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKASKRLREPLDGDGHESAEPYAKHMKP
                                                                                                                                                                                                                                 FATEDBAWAFVRKSASPEVSEGHENQHGQESBAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                                                                                                                                                                                                              MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK
                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                               SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRRPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                      TNORAQIHAACKAIEOAKTONINKLVLYTDSMFTINGITNWVQGQKKNGWKTSAGKEVIN
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/note= "Included within this region are the
amino acid residues that form the catalytic
divalent cation binding site, and the basic
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                                                                                                                                                                                                                                                                                                                                                     Score 1510; DB 5;
Pred. No. 7e-145;
3; Mismatches 3;
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241

KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 286

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The present sequence is a mutant RNase H1 sequence. RNase H hydrolyses RNA in RNA-DNA hybrids, and the activity of RNase H1 is Mg+2 dependent and inhibited by both Mn+2 and the sulphydryl blocking agent N-ethylmaleimide. The amino acid sequence of human RNase H1 displays strong homology with RNase H1 from yeast, chicken, E. coli and mouse. This sequence was generated from the wild-type human RNase H1 sequence (ABB83371) by site-directed mutagenesis. It was found that although the conserved amino acid residues of the putative catalytic site and basic substrate-binding domain are required for RNase H activity, deletion of either the catalytic site or the basic substrate binding domain did not ablate binding to the heteroduplex substrate. This mutant exhibited an undetectable rate of cleavage of a heteroduplex substrate, i.e. the mutation ablated the cleavage activity of the enzyme. Note: The present
                                                                                                                                                                                                                                                                                                                  Novel human RNase H1 polypeptide comprising mutations compared to wild type human RNase H1 useful for inhibiting expression of selected protein by antisense oligonucleotide targeted to RNA encoding selected protein.
Sequence
                       mutation ablated the cleavage activity of the enzyme. Note: The pesequence was not shown in the specification, but was derived from wild-type human RNase HI sequence shown on Fig 1
                                                                                                                                                                                                                                                                                     Disclosure; Page; 39pp; English.
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/note= "Included within this region are the
amino acid residues that form the catalytic
divalent cation binding site, and the basic
binding domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Crooke ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Asp substituted by Asn'
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Query Match

97.5%;

Score 1508;

DB 5;

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RESULT 12
ABB03373
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                        Novel human RNase H1 polypeptide comprising mutations compared to wild type human RNase H1 useful for inhibiting expression of selected protein by antisense oligonucleotide targeted to RNA encoding selected protein.
                                                                                                                                 WPI; 2002-519372/55
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/note= "Included within this region are the conserved amino acid residues that form the catalytic site, the divalent cation binding site, and the basic substrate-binding domain"
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3; Mismatches 3;
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Disclosure;

Page; 39pp; English

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RESULT 13
ABB83372
ID ABB83
XX ABB83
XX ABB83
XX O4-SE
DT 04-SE
DX Mutar
XX Humar
XX Homo
OS Synth
XX Key
FH Regic
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Similarity 97.9%;
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/label= Region_III
/note= "Included within this region are the conserved amino acid residues that form the catalytic site, the divalent cation binding site, and the basic substrate-binding domain"
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                                                                                                       /label= Region_II
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Pred. No. 1.1e-144;
3; Mismatches 3;
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RESULT 14
ABB83376
ID ABB83
XX
AC ABB83

standard; protein; 286

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240 240 180

ABB83376; ABB83376

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                      TNQRAEIHAACKAIEQAKTQNINKLYLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                                                        SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKFRAGIGVYWGFGHFLNVGIRLFGRQ 180
                                                                                                                                                                                                                                                                                                               FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
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                           KEDFVALERLTQGMDIQWMIVPGHSGFIGNEEADRLAREGAKQSED
                                                                                        TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGQAANGWKTSAGKEVIN
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KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
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Pred. No. 5.8e-144;
2; Mismatches 5;
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CC The present sequence is a mutant RNase H1 sequence. RNase H hydrolyses CC RNA in RNA-DNA hybrids, and the activity of RNase H1 is Mg+2 dependent CC and inhibited by both Mn+2 and the sulphydryl blocking agent N-CC ethylmaleimide. The amino acid sequence of human RNase H1 displays strong CC homology with RNase H1 from yeast, Chicken, E. coli and mouse. This CC sequence was generated from the wild-type human RNase H1 sequence CC (ABB3371) by site-directed mutagenesis. It was found that although the CC conserved amino acid residues of the putative catalytic site and basic CC substrate-binding domain are required for RNase H activity, deletion of CC either the catalytic site or the basic substrate-binding domain did not CC conserved amino acid residues of the putative catalytic sequence was not shown in the specification, but-was derived from the CCC wild-type human RNase H1 sequence shown on Fig 1
Query Match
Best Local S
Matches 277
                                                                                   Sequence
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    al Similarity
277; Conserv
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  96.3%;
|larity 96.9%;
|Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Contains the motif"
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/note= "Included within this region are the /note= "Included that form the catalytic amino acid residues that form the basic
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Score 1489; DB 5;
Pred. No. 9.7e-143;
2; Mismatches 7;
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RESULT 15
ADC39108
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09-MAY-2001

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22-MAY-2001

23-MAY-2001

23-MAY-2001

29-MAY-2001

29-MAY-2001

31-MAY-2001

31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic; nootropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive; antiarteriosclerotic; hemostatic; osteopathic; gene therapy.; NOVX; diabetes; obesity; cancer; hymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; wasting disorder; Alzheimer's disease; Parkinson's disorder; cachexia; cardiomyopathy; AIDS; asthma; Crohn's disease; multiple sclerosis; hypertension; atherosclerosis; hemophilia; graft-versus-host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-2002; 2002WO-US014199
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Albright here
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2003
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2001US-0299181BP
2001US-0290753BP
2001US-0290753BP
2001US-0291181P
2001US-0291181P
2001US-029101P
2001US-0292001P
2001US-0292370P
2001US-0293747P
2001US-0293747P
2001US-0294110P
2001US-0294110P
2001US-0294143P
2001US-029419P
2001US-039419P
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2001US-0314449P
2001US-03144463P
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2001US-0289087P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to new isolated NOVX polypeptides, the genes CC encoding them or sequences having at least 95% identity to the amino acid CC or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, CC particularly in the manufacture of a medicament for treating a syndrome CC associated with a human disease, which includes a pathology associated CC with NOVX polypeptide. The NOVX polypeptide is particularly useful for CC treating, preventing or alleviating pathology associated with NOVX polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and CC polypeptide are especially useful for treating or preventing e.g. CC diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate CC cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease, cardingtheses, anorexia, wasting disorders, Alzheimer's disease, conditiple sclerosis, hypertension, atherosclerosis, hemophilia, CC graft-versus-host disease or Albright hereditary osteodystrophy. The DNA CC conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic convertions. This sequence represents one of the NOVX proteins of the
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2001;
18-OCT-2001;
28-NOV-2001;
03-DEC-2001;
03-DEC-2001;
21-FEB-2002;
01-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New NOVX polypeptides and polynuclectides, useful in gene therapy, particularly for treating or preventing a syndrome associated with human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Padigaru M, l
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DB; ADC39107.
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                                                                                  TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                                                          FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                                                                                                                                                                                                   MSRLLSLAARVALAALPCRR-SRGFGMFYAVRRGGKSAVFLTGNECKAQVDRFPAARFKK
                   KEDFVALERLTQGMDIQW-----MHVP 262
                                                                TNQRAEIHAACKAIEQAQTQKINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                                    FATEDEAWDFVRKSASPEVSEGQENQHGQESETKASKRLREPLDGDGDESAEPYASTMKP
KEDFVALERLTQGMDIQWASILNVHVP 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2001US-0325683P.
; 2001US-0330292P.
; 2001US-0333873P.
; 2001US-0336909P.
; 2001US-0337552P.
; 2002US-0359245P.
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                     Score 1218; DB 7;
Pred. No. 3.4e-115;
7; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                     Length 269;
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for promoting the inhibition of the expression of a protein comprising employing a mammalian RNase H polypeptide so that cleavage of an RNA strand of an oligonucleotide-RNA complex duplex occurs. Also described is a compound 8 to 50 nucleobases in length targeted to the nucleic acid encoding the human RNase HI polypeptide, where the compound specifically hybridises with and inhibits the expression of a human RNase HI polypeptide. The compound, which is an antisense oligonucleotide, is useful for inhibiting the expression of a human RNase HII polypeptide in cells or tissues, as well as for treating an animal with a disease or condition associated with a human RNase HII polypeptide. The method is useful for inhibiting the expression of a protein, particularly for reducing cellular RNA via antisense technology. The present sequence represents a mouse RNase HI protein sequence, given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of a mammalian, particularly human, RNase H, for treating an with a disease or condition associated with a human RNase H, for inhibiting the expression of a protein, or for reducing cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse RNase HI protein sequence SEQ ID NO:11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-657606/70
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TNQRABIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                  DTEPAAVVSKDTFSYMGESVIVYTDGCCSSNGRKRARAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                         SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                                                                                                                        FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
                                                                                                                                                                                                                                                                                                                                                                       MRWLLPLSRTVTLAVVRLRRGICGLGMFYAVRRGRRTGVFLSWSECKAQVDRFPAARFKK
                                                                                                                                                                                                                                                                                                                                                                                                                 MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFFAARFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 60-61; 70pp; English
                                                                                                                                                                                                                                        FATEDEAWAFVRSSSSPDGSKGQESAHEQKSQAKTSKRPREPL-GEGEELPEPGPKHTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lima WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.5%; Score 1197.5; DB 5; 77.3%; Pred. No. 4.5e-113; tive 27; Mismatches 37;
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animal RNA via

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KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 286

TNQRAEIHAACKAIMQAKAQNISKLVLYTDSMFTINGITNWVQGWKKNGWRTSTGKDVIN

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179 180 119

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ADAO5718

ID ADAO5728

ADAO5718

AC ADAO5

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19-APR-2002;
19-APR-2002;
22-APR-2002;
16-MAY-2002;
16-MAY-2002;
16-MAY-2002;
17-MAY-2002;
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12-CCT-2001
15-CCT-2001
15-CCT-2001
17-CCT-2001
18-CCT-2001
24-CCT-2001
24-CCT-2001
24-CCT-2001
29-CCT-2001
29-CCT-2001
19-APR-2002
19-APR-2002
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05-OCT-2001;
05-OCT-2001;
09-OCT-2001;
09-OCT-2001;
                                                                                                                       Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar U Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Cattert Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Di Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
New NOVX polypeptides and nucleic acids, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2002; 2002WO-US031373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; NOVX; antidiabetic;
                                                       2003-381626/36
)B; ADA05717.
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2001US-0327435P.
2001US-0327917P.
2001US-0328049P.
2001US-0328049P.
2001US-0328049P.
2001US-0329414P.
2001US-033914058P.
2001US-03341058P.
2001US-0341058P.
2001US-0341058P.
2001US-03455P.
2001US-0343629P.
2001US-0343629P.
2001US-0343629P.
2001US-0343629P.
2001US-0343629P.
2001US-0343629P.
2002US-0343629P.
2002US-0343629P.
2002US-0346357P.
2002US-0373817P.
2002US-0373817P.
2002US-0373817P.
2002US-0373817P.
2002US-0373817P.
2002US-0373817P.
2002US-038164P.
2002US-0381642P.
2002US-0381642P.
2002US-0381642P.
2002US-0383656P.
2002US-0383658P.
2002US-038335P.
2002US-038335P.
2002US-038335P.
2002US-038335P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anorectic; antibacterial; virucide;
                                                                                                                                                                                                 Malyankar UM;
M, Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
                                                                                                                                                                                                                                                         Guo
                                                                                                                                                    Dipippo VA;
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pharmacogenomics.
                                                                                                                                                            preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
                                                                                                                                                Claim 1; Page 159; 586pp; English
                                                                                                                                                             obesity,
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CC (e.g. NOVI). Also described: (1) a composition comprising a polypeptide containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector CC comprising the nucleic acid molecule described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector CC comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically CC binds to the polypeptide described above; (7) methods for determining the comprising the presence of or predisposition to CC gample; (8) methods for determining the presence of or predisposition to CC adherence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a CC method of identifying an agent that binds to the polypeptide described above; (10) a method of identifying an agent that binds to the polypeptide described CC above; (10) a method for identifying a potential therapeutic agent for CC user and thysiological interactions of the polypeptide described CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method for modulating CC immunomodulator, cytostatic, nortcopic, natipating the above polypeptide in a CC acid molecule may be used to diagnose, treat or preventing an ind (14) a method for producing the above polypeptide in a CC syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic CC acid molecule may be used to diagnose, treat or prevent metabolic constructions of the polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic constructions. The nucleic acids can also be used as hybridiatation concer, and an interaction and various concer, and an interaction and the present sequence represents a human NOVX from the present sequence represents a human NOVX from the present t The present invention describes NOVX proteins, where X can be 1

Sequence 203 AA;

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158
                                                                            181
                                                                                                                                121 SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQ
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                                                                                                                                                            47
                                                                                                                                                                                    61 FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP 120
                                                                                                                                                                                                                              1 MSWLLFLAHRVALAALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK
                                                                                                                                                                                                                                                                                  Similarity
                                                                  TNORAEIHAACKAIEQAKTONINKLYLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
               KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 286
KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
                                                  TNQRAEIHAACKAIEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                                                                                                    Conservative
                                                                                                      -RDTFSYMGDFVVVYTDGCCSSNGRRRPRAGIGVYMGPGHPLNVGIRLPGRQ
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RESULT 18 ADA05720

ADA05720 standard; protein; 210

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06-NOV-2003

(first entry)

NOV15b

protein

ij

NO: 80

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22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
24-OCT-2001;
29-OCT-2001;
01-NOV-2001;
17-APR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-0CT-2001;
05-0CT-2001;
05-0CT-2001;
09-0CT-2001;
09-0CT-2001;
09-0CT-2001;
12-0CT-2001;
15-0CT-2001;
15-0CT-2001;
16-0CT-2001;
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19-APR-2002;
19-APR-2002;
22-APR-2002;
16-MAY-2002;
16-MAY-2002;
11-MAY-2002;
17-MAY-2002;
28-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; generapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                           New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
                                            Claim 1;
                                                                   pharmacogenomics.
                                                                                                                                                                                                          Patturajan M,
                                                                                                                                                                                                                       Smithson
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                                                                                                                                                           theon G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
turajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
mkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
en AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                           2003-381626/36.
)B; ADA05719.
                                                                                                                                                     J RA, NULL
J. Gangolli
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                                            Page 159;
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2002US-0381043P.
2002US-0381042P.
2002US-0383656P.
2002US-0383831P.
2002US-0393335P.
2002US-0393335P.
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2001US-0339266P
2001US-0343629P
2001US-0349575P
2001US-0349575P
2002US-0373260P
2002US-0373815P
2002US-0373817P
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2002US-0373817P
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2001US-0330142P.
2001US-0330309P.
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2001US-0328044P.
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                                            586pp;
                                          English.
                                                                                                                                                                                                    Malyankar UM;
                                                                               obesity,
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CC containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector CC comprising the above vector; (6) an antibody that immunospecifically CC binds to the polypeptide described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically CC binds to the polypeptide described above; (7) methods for determining the presence of or predisposition to CC sample; (8) methods for determining the presence of or predisposition to CC a disease associated with altered levels of expression of the above cCC adservant physiological interactions of the polypeptide described CC use in treating a pathology that is related to an aberrant expression or CC aberrant physiological interactions of the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the polypeptide; (12) a method of CC apathology associated with the above polypeptide in a CC syndrome associated with a human disease. The polypeptide of treating a CC syndrome associated with a human disease. The polypeptide or the nucleic CC disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's CC dyslipidaemias. The nucleic acids can also be used as hybridisation and can be used an shybridisation and can be used an shybridisation and pharmacogenomics. The present sequence represents a human NOVX from the pharmacogenomics. The present sequence represents a human NOVX from the
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Best Local (
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  162
                                     241
                                                                              102
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                     MSWILFLAHRVALAALFCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKK
                      KEDFVALERLTQGMDIQWMHVPGHSGFIGNEEADRLAREGAKQSED
                                                                                                   TNQRAEIHAACKAIEQAKTQNINKLYLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                SVEPAPPVSRDTFSYMGDFVVVYTDGCCSSNGRRKPRAGIGVYMGPGHPLNVGIRLPGRQ
KEDFVALERLTQGMDTQWMHVPGHSGFTGNEEADRLAREGAKQSED
                                                                              TNORAEIHAACKAIEQAKTONINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVIN
                                                                                                                                                                                                                                                                                  FATEDEAWAFVRKSASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKP
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä,
                                                                                                                                                             RDTFSYMGDFVVVYTDGCCSSNGRRRPRAGIGVYWGPGHPLNVGIRLPGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                           67.6%;
                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 1045.5; DB Pred. No. 8.7e-98; 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              6;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                              210;
                                                                                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                     180
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                                                                                                                        240
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RESULT 19
ADA05722
ID ADA05
XX ADA05
XX ADA05
XX ADA05
XX Human
XX Human
XX human
XX human
XX immun
XW immun
XW immun
XW antig
KW antig
human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaermic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
                                                                                                                06-NOV-2003
                                                                                                                                               ADA05722;
                                                                                                                                                                             ADA05722 standard;
                                                                               protein
                                                                                                               (first entry)
                                                                                                                                                                             protein; 195
                                                                               SEQ
                                                                                ä
                                                                                NO:82.
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described above

present invention describes NOVX proteins, where X can be 1 to 55 g. NOV1). Also described: (1) a composition comprising a polypeptide cribed above and a carrier; (2) a kit comprising, in one or more

The

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02-OCT-2001

05-OCT-2001

09-OCT-2001

09-OCT-2001

09-OCT-2001

11-OCT-2001

11-OCT-2001

11-OCT-2001

12-OCT-2001

12-OCT-2001

12-OCT-2001

24-OCT-2001

24-OCT-2001

24-OCT-2001

24-OCT-2001

17-APR-2002

11-APR-2002

11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0328849P.
2001US-0330142P.
2001US-033012P.
2001US-033030P.
2001US-0343629P.
2001US-034635P.
2001US-034635P.
2002US-0373815P.
2002US-0373826P.
2002US-0373826P.
2002US-0373826P.
2002US-0373826P.
2002US-0373826P.
2002US-0373826P.
2002US-0373826P.
2002US-03864P.
2002US-038164P.
2002US-038164P.
2002US-038164P.
2002US-038164P.
2002US-038164P.
2002US-0381638P.
2002US-0381642P.
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2001US-0327435P
2001US-0327449P
2001US-0327917P
2001US-0327917P
2001US-0328044P
2001US-0328046P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002WO-US031373
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Dipippo VA;

2003-381626/36. DB; ADA05721.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics. obesity,

Claim 1; Page 160; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

cc method of identifying an agent that binds to the polypeptide described cabove; (10) a method for identifying a potential theragentic agent for use in treating a pathology that is related to an aberrant expression or cc aberrant physiological interactions of the polypeptide; (11) a method of cc ereening for a modulator of activity or of latency or predisposition to ca pathology associated with the polypeptide; (12) a method for modulating cc recenting a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian cand antilipaemic activities, and can be used in gene therapy. The cc syndrome associated with a human disease. The polypeptide or the nucleic sold molecule may be used to diagnose, treat or prevent metabolic clisorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's clisease, immune disorders, haematopoietic disorders and various colds can also be used as hybridiastion and probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

Sequence 195 AA;

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Matches
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Best Local :
                          254
                                                         100
                                                                                     194
                                                                                                                                    134 SYMGDFVVVYTDGCCSSNGRRKPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKA
                                                                                                                    40
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                                                                                                                                                                                                         74
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                                                                                                                                                                                                                                                                                                188;
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                                                                                                                                                                                                                                                                                                              Similarity
                                                                       IEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQG
                                                                                                                  SYMGDFVVVYTDGCCSSNGRRRPRAGIGVYWGPGHPLNVGIRLPGRQTNQRAEIHAACKA
                                                                                                                                                                                                        SASPEVSEGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKPSVEPAPPVSRDTF
                                                                                                                                                                                                                                                      AALPCRRGSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFVRK
                 MDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 286
                                                       IEQAKTQNINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQG
                                                                                                                                                                                                                                     SALPCRRGSRGFGMFYAVRRGRKTGVFLTWNEC-----
MDIQWMHVPGHSGFIGNEEADRLAREGAKQSED 192
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                             63.4%;
                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                               Score 979.5; DB (
Pred. No. 4.1e-91;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                           6,
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                                                                                                                                                                                                                                                                                               83;
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                                                                                                                                                                                                                                                                                               Gaps
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AAY25098 standard; protein; 216

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24-AUG-1999 (first entry)

Mouse RNase H homologue protein fragment

Type N RNase H; oligonucleotide-RNA duplex; cleavage; target mRNA; mouse. antisense therapy;

WO9928447-A1

10-JUN-1999

RESULT 20
RAYZ5098
ID AAYZ5098
ID AAYX
XX AAYX
XX AAYX
XX AAYX
DT 24-J
DT 24-J
DT 17-DX
XX MOUS
XX MUS
XX MUS
PF 02-I
PF 02-I
PF 04-I 02-DEC-1998; 98WO-US025488

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ARESULT 21
AAAB97511
ID AAB97
XX
AC AAB97
XX
AC AAB97
XX
II 4-AU
XX
E col
XX
G E col
XX

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Best Local Similarity
Matches 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  duplexes and to develop agents for enhancing the efficiency of antisense therapy. The products of the invention are useful in defining the interaction of human Type 2 RNase H and antisense oligonucleotides and identifying methods for enhancing this interaction so that antisense oligonucleotides are more effective at inhibiting their target mRNA. The products can be used for enhancing the efficacy of antisense oligonucleotide therapies. This sequence represents a mouse RNase H homologue described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                     E coli type II RNase H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB97511 standard; protein; 216 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human RNase H polypeptide agents for enhancing the efficiency of
(ISIS-) ISIS PHARM INC
                                                      30-SEP-1999;
                                                                                                                29-SEP-2000; 2000WO-US026729
                                                                                                                                                                                                                                   WO200123613-A1
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                                                                                                                                                                                                                                                                                                                                                                              coli; RNase H type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes a novel human RNase H polypeptide and nucleic which can be used to cleave the RNA strand of oligonucleotide-RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
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IPGHSGFVGNEE 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NINKLVLYTDSMFTINGITNWVQGWKKNGWKTSAGKEVINKEDFVALERLTQGMDIQWMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSRGFGMFYAVRRGRKTGVFLTWNECRAQVDRFPAARFKKFATEDEAWAFVRKSASPEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGQESAHEQKSQAKTSKRPREPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGHENQHGQESEAKPGKRLREPLDGDGHESAQPYAKHMKPSVEPAPPVSRDTFSYMGDFV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GICGLGMFYAVRRGRRPGVFLSWSECKAQVDRFPAARFKKFATEDEAWAFVRSSSSPDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NISKLVLYTDSMFTINGITNWVQGWKKNGWRTSTGKDVINKEDFMELDELTQGMDIQWMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVYTDGCCSSNGRKRARAGIGVYWGPGHPLNVRIRLPGRQTNQRAEIHAACKAVMQAKAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry
                                                         99US-00409926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.0%;
                                                                                                                                                                                                                                                                                                                                                                              II; RNase H1 cleavage substrate; antisense therapy;
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Pred. No. 5.8e-89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and nucleic acid, used to develop antisense therapy.
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ARBSULT 22
ARB97509
ID ARB977
XX ARB97
XX ARB97
XX Chick
XX Chick
XX Chick
XX Gallu

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of DNA-RNA oligonuclectides which can act as substrates for human RNase HI (a type II RNase). The sequence consists of two portions, one owhich is capable of supporting cleavage of a complementary target RNA and the other of which is incapable of supporting such cleavage. These can be used to enhance the effectiveness of antisense therapies. The present sequence is E. coli RNase HI
                       WPI; 2001-343164/36
                                                                                                                                                                                                                                                                                                                                  WO200123613-A1
                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken; RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken type II RNase H protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB97509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 178pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric oligonucleotides that can serve as substrates for human RNase H1, useful for enhancing the effectiveness of antisense gene therapies
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                                                                          Crooke ST, Lima WF,
                                                                                                                                                                             30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2001
                                                                                                                                                                                                                             29-SEP-2000; 2000WO-US026729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy.
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                                                                                                                             SISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPGHSGFVGNEE 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGQESAHEQKSQAKTSKRPREPL-----V
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                                                                                                                             PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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Pred. No. 5.8e-89;
20; Mismatches 19
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                                                                             Manoharan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               cleavage substrate; antisense therapy;
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Matches 173
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                                                                              New isolated human RNase H polypeptide and nucleic acid, used agents for enhancing the efficiency of antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken type 2 RNase H protein
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                                                                                                                                                              WPI; 1999-394857/33.
                                                                                                                                                                                                                                                                                                                           04-DEC-1997;
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                                                                                                                                                                                                                      ST,
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                         Page
                                                                                                                                                                                                                   Lima WF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H; oligonucleotide-RNA duplex; cleavage; antisense therapy;
target mRNA; chicken; human.
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                                                                                                                                                                                                                                                                                                                           97US-0067458P
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                              29-30;
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                      37pp;
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Pred. No. 6.1e-81;
4; Mismatches 69
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RESULT 24
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Best Local S
Matches 172
    02-OCT-2001;
05-OCT-2001;
05-OCT-2001;
09-OCT-2001;
09-OCT-2001;
09-OCT-2001;
12-OCT-2001;
15-OCT-2001;
17-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
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2001US-0327435P.
2001US-0327947P.
2001US-032891P.
2001US-0328029P.
2001US-0328044P.
2001US-0328046P.
2001US-032844P.
2001US-0329414P.
2001US-0330142P.
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Pred. No. 9.7e
32; Mismatches
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No. 9.7e-81;
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CC (e.g. NOV1). Also described: (1) a composition comprising a polypeptide CC described above and a carrier; (2) a kit comprising in one or more CC containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector CC comprising the nucleic acid molecule described above; (5) acid to the polypeptide described above; (7) methods for determining the CC presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above; (8) methods for determining the presence of or predisposition to CC adisease associated with altered levels of expression of the above; (10) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for CC aberrant physiological interactions of the polypeptide; (11) a method of capability of a potential therapeutic agent for CC a pathology that is related to an aberrant expression or CC a pathology associated with the polypeptide; (11) a method of CC a pathology associated with the polypeptide; (12) a method for modulating CC immunomodulator; of activity or of latered polypeptide. NOVX CC sequences have antidiabetic, anotropic, neuroprotective, antiparkinsonian CC and antilipaemic activities, and can be used in gene therapy. The CC polypeptide is useful in manufacturing a medicament for treating a cCC syndrome associated with a human disease. The polypeptide or the nucleic disorders such as Alzheimer's disease or Parkinson's CCC disease, incurance disorders such as Alzheimer's disease or Parkinson's CCC disease, incurance adisorders, haematopoietic disorders and various of probes, in chromosome mapping, tissue typing, preventive medicitie and cprobes, in chromosome mapping, tissue typing, preventive medicitie and cprobes in a present sequence represents a human NOVX from the
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01-NOV-2001;
17-APR-2002;
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Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CB, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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16-MAY-2002;
17-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
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16-MAY-2002;
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2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
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2002US-0381042P.
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2002US-0391335P.
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2002US-0373815P.
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o R

Query Match Best Local Similarity

27.3%;

Score 422; DB 4; Pred. No. 4.8e-34;

18

Sequence 333

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                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating chila signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                              Disclosure; SEQ ID NO 2112; 21pp + Sequence Listing; English
                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL02543.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                          genes from Drosophila interactions.
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315 EMADKLARQGS 325
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